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GI 6055-64X

SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

5 This application is a continuation-in-part of the following applications:

- (1) Ser. No. 09/197,886 (GI 6055A), filed November 23, 1998; which is a continuation-in-part of provisional application Ser. No. 60/126,425 (GI 6055), filed November 26, 1997, now abandoned;
- 10 (2) Ser. No. 09/203,106 (GI 6056A), filed November 30, 1998; which is a continuation-in-part of provisional application Ser. No. 60/067,454 (GI 6056), filed December 4, 1997, now abandoned;
- (3) Ser. No. 09/212,843 (GI 6057A), filed December 16, 1998; which is a continuation-in-part of provisional application Ser. No. 60/068,379 (GI 6057), filed December 20, 1997, now abandoned;
- 15 (4) Ser. No. 09/222,653 (GI 6058A), filed December 30, 1998; which is a continuation-in-part of provisional application Ser. No. 60/070,346 (GI 6058), filed January 2, 1998, now abandoned;
- (5) Ser. No. 09/225,049 (GI 6059A), filed January 4, 1999; which is a continuation-in-part of provisional application Ser. No. 60/070,643 (GI 6059), filed January 7, 1998, now abandoned;
- 20 (6) Ser. No. 09/225,585 (GI 6060A), filed January 6, 1999; which is a continuation-in-part of provisional application Ser. No. 60/070,755 (GI 6060), filed January 8, 1998, now abandoned;
- 25 (7) Ser. No. 09/227,462 (GI 6061A), filed January 8, 1999; which is a continuation-in-part of provisional application Ser. No. 60/071,304 (GI 6061), filed January 13, 1998, now abandoned;

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- (8) Ser. No. 09/235,609 (GI 6062A), filed January 20, 1999; which is a continuation-in-part of provisional application Ser. No. 60/072,134 (GI 6062), filed January 22, 1998, now abandoned;
- (9) Ser. No. 09/237,847 (GI 6063A), filed January 27, 1999; which is a continuation-in-part of provisional application Ser. No. 60/073,095 (GI 6063), filed January 30, 1998, now abandoned;
- (10) Ser. No. 09/251,600 (GI 6064A), filed February 17, 1999; which is a continuation-in-part of provisional application Ser. No. 60/075,038 (GI 6064), filed February 18, 1998, now abandoned;
- all of which are incorporated by reference herein.

FIELD OF THE INVENTION

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

BACKGROUND OF THE INVENTION

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 63 to nucleotide 1265;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 132 to nucleotide 1265;

10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bd306_7 deposited with the ATCC under accession number 98599;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bd306_7 deposited with the ATCC under accession number 98599;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bd306_7 deposited with the ATCC under accession number 98599;

20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bd306_7 deposited with the ATCC under accession number 98599;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:2;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 63 to nucleotide 1265; the nucleotide sequence of SEQ ID NO:1

from nucleotide 132 to nucleotide 1265; the nucleotide sequence of the full-length protein coding sequence of clone bd306_7 deposited with the ATCC under accession number 98599; or the nucleotide sequence of a mature protein coding sequence of clone bd306_7 deposited with the ATCC under accession number 98599. In other preferred
5 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bd306_7 deposited with the ATCC under accession number 98599. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2 from amino acid 148 to amino acid 189. In further preferred embodiments, the present
10 invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment
15 comprising the amino acid sequence from amino acid 195 to amino acid 204 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

Further embodiments of the invention provide isolated polynucleotides produced
20 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
25 (aa) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and
 (ab) the nucleotide sequence of the cDNA insert of clone bd306_7 deposited with the ATCC under accession number 98599; and
30 (ii) hybridizing said probe(s) to human DNA; and
 (iii) isolating the DNA polynucleotide detected with the probe(s);
 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

(bb) the nucleotide sequence of the cDNA insert of clone bd306_7 deposited with the ATCC under accession number 98599; and

10 (ii) hybridizing said primer(s) to human DNA;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 63 to nucleotide
20 1265, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 63 to nucleotide 1265, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 63 to nucleotide 1265. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
25 NO:1 from nucleotide 132 to nucleotide 1265, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 132 to nucleotide 1265, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 132 to nucleotide 1265.

In other embodiments, the present invention provides a composition comprising
30 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:2;

(b) the amino acid sequence of SEQ ID NO:2 from amino acid 148 to amino acid 189;

(c) fragments of the amino acid sequence of SEQ ID NO:2 comprising eight consecutive amino acids of SEQ ID NO:2; and

5 (d) the amino acid sequence encoded by the cDNA insert of clone bd306_7 deposited with the ATCC under accession number 98599;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2 or the amino acid sequence of SEQ ID NO:2 from amino acid 148 to amino acid 189. In further preferred
10 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:2, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid
15 sequence from amino acid 195 to amino acid 204 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;

20 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 719 to nucleotide 1855;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 779 to nucleotide 1855;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fj283_11 deposited with the ATCC under
25 accession number 98599;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fj283_11 deposited with the ATCC under accession number 98599;

30 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fj283_11 deposited with the ATCC under accession number 98599;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fj283_11 deposited with the ATCC under accession number 98599;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;

5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:4;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
15 NO:3 from nucleotide 719 to nucleotide 1855; the nucleotide sequence of SEQ ID NO:3 from nucleotide 779 to nucleotide 1855; the nucleotide sequence of the full-length protein coding sequence of clone fj283_11 deposited with the ATCC under accession number 98599; or the nucleotide sequence of a mature protein coding sequence of clone fj283_11 deposited with the ATCC under accession number 98599. In other preferred
20 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fj283_11 deposited with the ATCC under accession number 98599. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4 from amino acid 1 to amino acid 27. In further preferred embodiments, the present
25 invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:4, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment
30 comprising the amino acid sequence from amino acid 184 to amino acid 193 of SEQ ID NO:4.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:3.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(ab) the nucleotide sequence of the cDNA insert of clone fj283_11 deposited with the ATCC under accession number 98599; and

(ii) hybridizing said probe(s) to human DNA; and

(iii) isolating the DNA polynucleotide detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(bb) the nucleotide sequence of the cDNA insert of clone fj283_11 deposited with the ATCC under accession number 98599; and

(ii) hybridizing said primer(s) to human DNA;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:3 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 719 to nucleotide 1855, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 719 to nucleotide 1855, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 719 to nucleotide 1855. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 779 to nucleotide 1855, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 779 to nucleotide 1855, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 779 to nucleotide 1855.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:4;
- (b) the amino acid sequence of SEQ ID NO:4 from amino acid 1 to amino acid 27;
- (c) fragments of the amino acid sequence of SEQ ID NO:4 comprising eight consecutive amino acids of SEQ ID NO:4;
- (d) the amino acid sequence encoded by the cDNA insert of clone fj283_11 deposited with the ATCC under accession number 98599; and
- (e) the amino acid sequence encoded by the cDNA insert of clone fj283_6 deposited with the ATCC under accession number xxxxx;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4 or the amino acid sequence of SEQ ID NO:4 from amino acid 1 to amino acid 27. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:4, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 184 to amino acid 193 of SEQ ID NO:4.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:198;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:198 from nucleotide 982 to nucleotide 2118;

5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:198 from nucleotide 1042 to nucleotide 2118;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:198 from nucleotide 621 to nucleotide 1248;

10 (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fj283_6 deposited with the ATCC under accession number 98988;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fj283_6 deposited with the ATCC under accession number 98988;

15 (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fj283_6 deposited with the ATCC under accession number 98988;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fj283_6 deposited with the ATCC under accession number 98988;

20 (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:4;

25 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and

30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:198 from nucleotide 982 to nucleotide 2118; the nucleotide sequence of SEQ ID NO:198 from nucleotide 1042 to nucleotide 2118; the nucleotide sequence of SEQ ID

NO:198 from nucleotide 621 to nucleotide 1248; the nucleotide sequence of the full-length protein coding sequence of clone fj283_6 deposited with the ATCC under accession number 98988; or the nucleotide sequence of a mature protein coding sequence of clone fj283_6 deposited with the ATCC under accession number 98988. In other preferred
5 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fj283_6 deposited with the ATCC under accession number 98988. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more
10 preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:4, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 184 to amino acid 193 of SEQ ID NO:4.

Other embodiments provide the gene corresponding to the cDNA sequence of
15 SEQ ID NO:198.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:
 (i) preparing one or more polynucleotide probes that hybridize
20 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

 (aa) SEQ ID NO:198, but excluding the poly(A) tail at the
 3' end of SEQ ID NO:198; and

 (ab) the nucleotide sequence of the cDNA insert of clone
25 fj283_6 deposited with the ATCC under accession number 98988;
 and

 (ii) hybridizing said probe(s) to human DNA; and
 (iii) isolating the DNA polynucleotide detected with the
 probe(s);

30 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:198, but excluding the poly(A) tail at the 3' end of SEQ ID NO:198; and
- (bb) the nucleotide sequence of the cDNA insert of clone f283_6 deposited with the ATCC under accession number 98988; and
- (ii) hybridizing said primer(s) to human DNA;
- 10 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:198, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
15 ID NO:198 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:198, but excluding the poly(A) tail at the 3' end of SEQ ID NO:198. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:198 from nucleotide 982 to nucleotide 2118, and extending contiguously from a nucleotide sequence corresponding
20 to the 5' end of said sequence of SEQ ID NO:198 from nucleotide 982 to nucleotide 2118, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:198 from nucleotide 982 to nucleotide 2118. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:198 from nucleotide 1042 to nucleotide 2118, and
25 extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:198 from nucleotide 1042 to nucleotide 2118, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:198 from nucleotide 1042 to nucleotide 2118. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of
30 SEQ ID NO:198 from nucleotide 621 to nucleotide 1248, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:198 from nucleotide 621 to nucleotide 1248, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:198 from nucleotide 621 to nucleotide 1248.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 259 to nucleotide 624;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fk317_3 deposited with the ATCC under accession number 98599;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fk317_3 deposited with the ATCC under accession number 98599;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fk317_3 deposited with the ATCC under
15 accession number 98599;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fk317_3 deposited with the ATCC under accession number 98599;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- 20 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:6;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 25 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
30 NO:5 from nucleotide 259 to nucleotide 624; the nucleotide sequence of the full-length protein coding sequence of clone fk317_3 deposited with the ATCC under accession number 98599; or the nucleotide sequence of a mature protein coding sequence of clone fk317_3 deposited with the ATCC under accession number 98599. In other preferred

embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fk317_3 deposited with the ATCC under accession number 98599. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6 from amino acid 1 to amino acid 72. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:6, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 56 to amino acid 65 of SEQ ID NO:6.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:5.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

- (ab) the nucleotide sequence of the cDNA insert of clone fk317_3 deposited with the ATCC under accession number 98599;

and

- (ii) hybridizing said probe(s) to human DNA; and
 - (iii) isolating the DNA polynucleotide detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(bb) the nucleotide sequence of the cDNA insert of clone fk317_3 deposited with the ATCC under accession number 98599;

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and

(ii) hybridizing said primer(s) to human DNA;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:5 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 259 to nucleotide 624, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 259 to nucleotide 624, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 259 to nucleotide 624.

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In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:6;

(b) the amino acid sequence of SEQ ID NO:6 from amino acid 1 to amino acid 72;

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(c) fragments of the amino acid sequence of SEQ ID NO:6 comprising eight consecutive amino acids of SEQ ID NO:6; and

(d) the amino acid sequence encoded by the cDNA insert of clone fk317_3 deposited with the ATCC under accession number 98599;

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the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:6 or the amino acid sequence of SEQ ID NO:6 from amino acid 1 to amino acid 72. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid

sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:6, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 56 to amino acid 65 of SEQ ID NO:6.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 357 to nucleotide 578;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 471 to nucleotide 578;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone k213_2x deposited with the ATCC under accession number 98599;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone k213_2x deposited with the ATCC under accession number 98599;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone k213_2x deposited with the ATCC under accession number 98599;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone k213_2x deposited with the ATCC under accession number 98599;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:8;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 357 to nucleotide 578; the nucleotide sequence of SEQ ID NO:7 from nucleotide 471 to nucleotide 578; the nucleotide sequence of the full-length protein coding sequence of clone k213_2x deposited with the ATCC under accession number 98599; or the nucleotide sequence of a mature protein coding sequence of clone k213_2x deposited with the ATCC under accession number 98599. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone k213_2x deposited with the ATCC under accession number 98599. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:8, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:8.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

(ab) the nucleotide sequence of the cDNA insert of clone k213_2x deposited with the ATCC under accession number 98599; and

(ii) hybridizing said probe(s) to human DNA; and

(iii) isolating the DNA polynucleotide detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

(bb) the nucleotide sequence of the cDNA insert of clone k213_2x deposited with the ATCC under accession number 98599;

and

(ii) hybridizing said primer(s) to human DNA;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 357 to nucleotide 578, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 357 to nucleotide 578, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 357 to nucleotide 578. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 471 to nucleotide 578, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 471 to nucleotide 578, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 471 to nucleotide 578.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:8;

(b) fragments of the amino acid sequence of SEQ ID NO:8 comprising eight consecutive amino acids of SEQ ID NO:8; and

(c) the amino acid sequence encoded by the cDNA insert of clone k213_2x deposited with the ATCC under accession number 98599;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino
10 acids of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 332 to nucleotide 598;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 458 to nucleotide 598;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone na316_1 deposited with the ATCC under accession number 98599;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone na316_1 deposited with the ATCC under accession number 98599;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone na316_1 deposited with the ATCC under accession number 98599;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone na316_1 deposited with the ATCC under accession number 98599;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:10;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9 from nucleotide 332 to nucleotide 598; the nucleotide sequence of SEQ ID NO:9 from nucleotide 458 to nucleotide 598; the nucleotide sequence of the full-length protein coding sequence of clone na316_1 deposited with the ATCC under accession number 98599; or the nucleotide sequence of a mature protein coding sequence of clone na316_1 deposited with the ATCC under accession number 98599. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone na316_1 deposited with the ATCC under accession number 98599. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:10, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:10.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:9.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(ab) the nucleotide sequence of the cDNA insert of clone na316_1 deposited with the ATCC under accession number 98599;

5

and

(ii) hybridizing said probe(s) to human DNA; and

(iii) isolating the DNA polynucleotide detected with the probe(s);

and

10

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15

(ba) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(bb) the nucleotide sequence of the cDNA insert of clone na316_1 deposited with the ATCC under accession number 98599; and

20

(ii) hybridizing said primer(s) to human DNA;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:9 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 332 to nucleotide 598, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 332 to nucleotide 598, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 332 to nucleotide 598. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:9 from nucleotide 458 to nucleotide 598, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 458 to nucleotide 598, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 458 to nucleotide 598.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
- (b) fragments of the amino acid sequence of SEQ ID NO:10 comprising
10 eight consecutive amino acids of SEQ ID NO:10; and
- (c) the amino acid sequence encoded by the cDNA insert of clone na316_1 deposited with the ATCC under accession number 98599;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:10. In further preferred
15 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:10, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid
20 sequence from amino acid 39 to amino acid 48 of SEQ ID NO:10.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:11 from nucleotide 354 to nucleotide 986;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 408 to nucleotide 986;
- (d) a polynucleotide comprising the nucleotide sequence of the full-
30 length protein coding sequence of clone nf93_20 deposited with the ATCC under accession number 98599;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone nf93_20 deposited with the ATCC under accession number 98599;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone nf93_20 deposited with the ATCC under accession number 98599;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone nf93_20 deposited with the ATCC under accession number 98599;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:12;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 354 to nucleotide 986; the nucleotide sequence of SEQ ID NO:11 from nucleotide 408 to nucleotide 986; the nucleotide sequence of the full-length protein coding sequence of clone nf93_20 deposited with the ATCC under accession number 98599; or the nucleotide sequence of a mature protein coding sequence of clone nf93_20 deposited with the ATCC under accession number 98599. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone nf93_20 deposited with the ATCC under accession number 98599. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:12, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence

of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 100 to amino acid 109 of SEQ ID NO:12.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(ab) the nucleotide sequence of the cDNA insert of clone nf93_20 deposited with the ATCC under accession number 98599; and

15 (ii) hybridizing said probe(s) to human DNA; and

(iii) isolating the DNA polynucleotide detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(bb) the nucleotide sequence of the cDNA insert of clone nf93_20 deposited with the ATCC under accession number 98599; and

(ii) hybridizing said primer(s) to human DNA;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11, and

extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:11 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
5 corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 354 to nucleotide 986, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 354 to nucleotide 986, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 354 to nucleotide 986. Also preferably the polynucleotide isolated according to the above
10 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 408 to nucleotide 986, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 408 to nucleotide 986, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 408 to nucleotide 986.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
- (b) fragments of the amino acid sequence of SEQ ID NO:12 comprising
20 eight consecutive amino acids of SEQ ID NO:12; and
- (c) the amino acid sequence encoded by the cDNA insert of clone nf93_20 deposited with the ATCC under accession number 98599;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12. In further preferred
25 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:12, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid
30 sequence from amino acid 100 to amino acid 109 of SEQ ID NO:12.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 301 to nucleotide 1821;

5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 1381 to nucleotide 1821;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone np164_1 deposited with the ATCC under accession number 98599;

10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone np164_1 deposited with the ATCC under accession number 98599;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone np164_1 deposited with the ATCC under
15 accession number 98599;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone np164_1 deposited with the ATCC under accession number 98599;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;

20 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:14;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

25 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
30 NO:13 from nucleotide 301 to nucleotide 1821; the nucleotide sequence of SEQ ID NO:13 from nucleotide 1381 to nucleotide 1821; the nucleotide sequence of the full-length protein coding sequence of clone np164_1 deposited with the ATCC under accession number 98599; or the nucleotide sequence of a mature protein coding sequence of clone

np164_1 deposited with the ATCC under accession number 98599. In other preferred
embodiments, the polynucleotide encodes the full-length or a mature protein encoded by
the cDNA insert of clone np164_1 deposited with the ATCC under accession number
98599. In further preferred embodiments, the present invention provides a
5 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more
preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:14, or
a polynucleotide encoding a protein comprising a fragment of the amino acid sequence
of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid
10 sequence from amino acid 248 to amino acid 257 of SEQ ID NO:14.

Other embodiments provide the gene corresponding to the cDNA sequence of
SEQ ID NO:13.

Further embodiments of the invention provide isolated polynucleotides produced
according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
consisting of:
 - (aa) SEQ ID NO:13, but excluding the poly(A) tail at the
20 3' end of SEQ ID NO:13; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
np164_1 deposited with the ATCC under accession number 98599;
and
 - (ii) hybridizing said probe(s) to human DNA; and
 - 25 (iii) isolating the DNA polynucleotide detected with the
probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that
30 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:
 - (ba) SEQ ID NO:13, but excluding the poly(A) tail at the
3' end of SEQ ID NO:13; and

(bb) the nucleotide sequence of the cDNA insert of clone np164_1 deposited with the ATCC under accession number 98599; and

(ii) hybridizing said primer(s) to human DNA;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
10 ID NO:13 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 301 to nucleotide 1821, and extending contiguously from a nucleotide sequence corresponding to the 5' end
15 of said sequence of SEQ ID NO:13 from nucleotide 301 to nucleotide 1821, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 301 to nucleotide 1821. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 1381 to nucleotide 1821, and extending contiguously from
20 a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 1381 to nucleotide 1821, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 1381 to nucleotide 1821.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the
25 group consisting of:

(a) the amino acid sequence of SEQ ID NO:14;

(b) fragments of the amino acid sequence of SEQ ID NO:14 comprising eight consecutive amino acids of SEQ ID NO:14; and

(c) the amino acid sequence encoded by the cDNA insert of clone np164_1 deposited with the ATCC under accession number 98599;
30

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:14. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:14, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid
5 sequence from amino acid 248 to amino acid 257 of SEQ ID NO:14.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 148 to nucleotide 537;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pe204_1 deposited with the ATCC under accession number 98599;
- 15 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pe204_1 deposited with the ATCC under accession number 98599;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pe204_1 deposited with the ATCC under
20 accession number 98599;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pe204_1 deposited with the ATCC under accession number 98599;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- 25 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:16;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- 30 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 148 to nucleotide 537; the nucleotide sequence of the full-length protein coding sequence of clone pe204_1 deposited with the ATCC under accession number 98599; or the nucleotide sequence of a mature protein coding sequence of clone pe204_1 deposited with the ATCC under accession number 98599. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pe204_1 deposited with the ATCC under accession number 98599. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 60 to amino acid 69 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and
 - (ab) the nucleotide sequence of the cDNA insert of clone pe204_1 deposited with the ATCC under accession number 98599; and
 - (ii) hybridizing said probe(s) to human DNA; and
 - (iii) isolating the DNA polynucleotide detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and
- (bb) the nucleotide sequence of the cDNA insert of clone pe204_1 deposited with the ATCC under accession number 98599; and
- (ii) hybridizing said primer(s) to human DNA;
- 10 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:15 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 148 to nucleotide 537, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 148 to nucleotide 537, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 148 to nucleotide 537.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
- (b) fragments of the amino acid sequence of SEQ ID NO:16 comprising eight consecutive amino acids of SEQ ID NO:16; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pe204_1 deposited with the ATCC under accession number 98599;

30 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid
5 sequence from amino acid 60 to amino acid 69 of SEQ ID NO:16.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 24 to nucleotide 1109;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 1050 to nucleotide 1109;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ya1_1 deposited with the ATCC under accession number 98599;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ya1_1 deposited with the ATCC under accession number 98599;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ya1_1 deposited with the ATCC under accession number 98599;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ya1_1 deposited with the ATCC under accession number 98599;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:18;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:17 from nucleotide 24 to nucleotide 1109; the nucleotide sequence of SEQ ID NO:17
5 from nucleotide 1050 to nucleotide 1109; the nucleotide sequence of the full-length protein coding sequence of clone ya1_1 deposited with the ATCC under accession number 98599; or the nucleotide sequence of a mature protein coding sequence of clone ya1_1 deposited with the ATCC under accession number 98599. In other preferred
10 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ya1_1 deposited with the ATCC under accession number 98599.

In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:18, or a
15 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 176 to amino acid 185 of SEQ ID NO:18.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:17.

20 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
25 consisting of:

(aa) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

(ab) the nucleotide sequence of the cDNA insert of clone ya1_1 deposited with the ATCC under accession number 98599;
30 and

(ii) hybridizing said probe(s) to human DNA; and

(iii) isolating the DNA polynucleotide detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

(bb) the nucleotide sequence of the cDNA insert of clone ya1_1 deposited with the ATCC under accession number 98599; and

(ii) hybridizing said primer(s) to human DNA;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:17 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 24 to nucleotide 1109, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 24 to nucleotide 1109, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 24 to nucleotide 1109. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 1050 to nucleotide 1109, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 1050 to nucleotide 1109, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 1050 to nucleotide 1109.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:18;

(b) fragments of the amino acid sequence of SEQ ID NO:18 comprising eight consecutive amino acids of SEQ ID NO:18; and

(c) the amino acid sequence encoded by the cDNA insert of clone ya1_1 deposited with the ATCC under accession number 98599;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:18. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino
10 acids of SEQ ID NO:18, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 176 to amino acid 185 of SEQ ID NO:18.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 27 to nucleotide 734;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 270 to nucleotide 734;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 85 to nucleotide 1604;

25 (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb8_1 deposited with the ATCC under accession number 98599;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb8_1 deposited with the ATCC under accession number 98599;

30 (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb8_1 deposited with the ATCC under accession number 98599;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb8_1 deposited with the ATCC under accession number 98599;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:20;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:19 from nucleotide 27 to nucleotide 734; the nucleotide sequence of SEQ ID NO:19 from nucleotide 270 to nucleotide 734; the nucleotide sequence of SEQ ID NO:19 from nucleotide 85 to nucleotide 1604; the nucleotide sequence of the full-length protein coding sequence of clone yb8_1 deposited with the ATCC under accession number 98599; or the nucleotide sequence of a mature protein coding sequence of clone yb8_1 deposited with the ATCC under accession number 98599. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb8_1 deposited with the ATCC under accession number 98599. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20 from amino acid 70 to amino acid 236. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:20, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 113 to amino acid 122 of SEQ ID NO:20.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:19.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(ab) the nucleotide sequence of the cDNA insert of clone yb8_1 deposited with the ATCC under accession number 98599; and

10 (ii) hybridizing said probe(s) to human DNA; and

(iii) isolating the DNA polynucleotide detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

20 (bb) the nucleotide sequence of the cDNA insert of clone yb8_1 deposited with the ATCC under accession number 98599; and

(ii) hybridizing said primer(s) to human DNA;

(iii) amplifying human DNA sequences; and

25 (iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:19 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:19, but
30 excluding the poly(A) tail at the 3' end of SEQ ID NO:19. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 27 to nucleotide 734, and extending contiguously from a nucleotide sequence corresponding to the 5' end

of said sequence of SEQ ID NO:19 from nucleotide 27 to nucleotide 734, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 27 to nucleotide 734. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 270 to nucleotide 734, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 270 to nucleotide 734, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 270 to nucleotide 734. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 85 to nucleotide 1604, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 85 to nucleotide 1604, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 85 to nucleotide 1604.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:20;
- (b) the amino acid sequence of SEQ ID NO:20 from amino acid 70 to amino acid 236;
- (c) fragments of the amino acid sequence of SEQ ID NO:20 comprising eight consecutive amino acids of SEQ ID NO:20; and
- (d) the amino acid sequence encoded by the cDNA insert of clone yb8_1 deposited with the ATCC under accession number 98599;

25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:20 or the amino acid sequence of SEQ ID NO:20 from amino acid 70 to amino acid 236. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:20, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 113 to amino acid 122 of SEQ ID NO:20.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 469 to nucleotide 609;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 574 to nucleotide 609;
- 10 (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 214 to nucleotide 369;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone am856_3 deposited with the ATCC under accession number 98600;
- 15 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone am856_3 deposited with the ATCC under accession number 98600;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone am856_3 deposited with the ATCC under accession number 98600;
- 20 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone am856_3 deposited with the ATCC under accession number 98600;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
- 25 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:22;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- 30 (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:21 from nucleotide 469 to nucleotide 609; the nucleotide sequence of SEQ ID NO:21 from nucleotide 574 to nucleotide 609; the nucleotide sequence of SEQ ID NO:21 from nucleotide 214 to nucleotide 369; the nucleotide sequence of the full-length protein coding sequence of clone am856_3 deposited with the ATCC under accession number 98600; or the nucleotide sequence of a mature protein coding sequence of clone am856_3 deposited with the ATCC under accession number 98600. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone am856_3 deposited with the ATCC under accession number 98600. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:22 from amino acid 1 to amino acid 38. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:22, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 18 to amino acid 27 of SEQ ID NO:22.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:21.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and
 - (ab) the nucleotide sequence of the cDNA insert of clone am856_3 deposited with the ATCC under accession number 98600; and
 - (ii) hybridizing said probe(s) to human DNA; and

(iii) isolating the DNA polynucleotide detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

10 (bb) the nucleotide sequence of the cDNA insert of clone am856_3 deposited with the ATCC under accession number 98600; and

(ii) hybridizing said primer(s) to human DNA;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:21 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:21, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:21. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 469 to nucleotide 609, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 469 to nucleotide 609, to a nucleotide
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 469 to nucleotide 609. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 574 to nucleotide 609, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from
30 nucleotide 574 to nucleotide 609, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 574 to nucleotide 609. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 214 to

nucleotide 369, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 214 to nucleotide 369, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 214 to nucleotide 369.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:22;
 - (b) the amino acid sequence of SEQ ID NO:22 from amino acid 1 to
10 amino acid 38;
 - (c) fragments of the amino acid sequence of SEQ ID NO:22 comprising eight consecutive amino acids of SEQ ID NO:22; and
 - (d) the amino acid sequence encoded by the cDNA insert of clone am856_3 deposited with the ATCC under accession number 98600;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:22 or the amino acid sequence of SEQ ID NO:22 from amino acid 1 to amino acid 38. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising
20 eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:22, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 18 to amino acid 27 of SEQ ID NO:22.

In one embodiment, the present invention provides a composition comprising an
25 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 442 to nucleotide 735;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:23 from nucleotide 520 to nucleotide 735;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone am996_12 deposited with the ATCC under accession number 98600;

5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone am996_12 deposited with the ATCC under accession number 98600;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone am996_12 deposited with the ATCC under accession number 98600;

10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone am996_12 deposited with the ATCC under accession number 98600;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:24;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:24;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:23 from nucleotide 442 to nucleotide 735; the nucleotide sequence of SEQ ID NO:23
25 from nucleotide 520 to nucleotide 735; the nucleotide sequence of the full-length protein coding sequence of clone am996_12 deposited with the ATCC under accession number 98600; or the nucleotide sequence of a mature protein coding sequence of clone am996_12 deposited with the ATCC under accession number 98600. In other preferred
30 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone am996_12 deposited with the ATCC under accession number 98600. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:24 from amino acid 1 to amino acid 90. In further preferred embodiments, the present

invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:24, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:24.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:23.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(ab) the nucleotide sequence of the cDNA insert of clone am996_12 deposited with the ATCC under accession number 98600; and

(ii) hybridizing said probe(s) to human DNA; and

(iii) isolating the DNA polynucleotide detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(bb) the nucleotide sequence of the cDNA insert of clone am996_12 deposited with the ATCC under accession number 98600; and

- (ii) hybridizing said primer(s) to human DNA;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 442 to nucleotide 735, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 442 to nucleotide 735, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 442 to nucleotide 735. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 520 to nucleotide 735, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 520 to nucleotide 735, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 520 to nucleotide 735.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:24;
- (b) the amino acid sequence of SEQ ID NO:24 from amino acid 1 to amino acid 90;
- (c) fragments of the amino acid sequence of SEQ ID NO:24 comprising eight consecutive amino acids of SEQ ID NO:24; and
- (d) the amino acid sequence encoded by the cDNA insert of clone am996_12 deposited with the ATCC under accession number 98600;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:24 or the amino acid sequence of SEQ ID NO:24 from amino acid 1 to amino acid 90. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid

sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:24, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:24.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 127 to nucleotide 240;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cc69_1 deposited with the ATCC under accession number 98600;
- 15 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cc69_1 deposited with the ATCC under accession number 98600;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cc69_1 deposited with the ATCC under accession number 98600;
- 20 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cc69_1 deposited with the ATCC under accession number 98600;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:26;
- 25 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:26;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 30 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:25 from nucleotide 127 to nucleotide 240; the nucleotide sequence of the full-length protein coding sequence of clone cc69_1 deposited with the ATCC under accession number 98600; or the nucleotide sequence of a mature protein coding sequence of clone
5 cc69_1 deposited with the ATCC under accession number 98600. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cc69_1 deposited with the ATCC under accession number 98600.

In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26
10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:26, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 14 to amino acid 23 of SEQ ID NO:26.

15 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:25.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 20 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and
 - 25 (ab) the nucleotide sequence of the cDNA insert of clone cc69_1 deposited with the ATCC under accession number 98600; and
 - (ii) hybridizing said probe(s) to human DNA; and
 - (iii) isolating the DNA polynucleotide detected with the
30 probe(s);
 - and
 - (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and
- (bb) the nucleotide sequence of the cDNA insert of clone cc69_1 deposited with the ATCC under accession number 98600; and
- (ii) hybridizing said primer(s) to human DNA;
- 10 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
15 ID NO:25 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 127 to nucleotide 240, and extending contiguously from a nucleotide sequence corresponding to the 5' end
20 of said sequence of SEQ ID NO:25 from nucleotide 127 to nucleotide 240, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 127 to nucleotide 240.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the
25 group consisting of:

- (a) the amino acid sequence of SEQ ID NO:26;
- (b) fragments of the amino acid sequence of SEQ ID NO:26 comprising eight consecutive amino acids of SEQ ID NO:26; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
30 cc69_1 deposited with the ATCC under accession number 98600;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:26. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:26, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid
5 sequence from amino acid 14 to amino acid 23 of SEQ ID NO:26.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 156 to nucleotide 413;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 198 to nucleotide 413;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cc162_1 deposited with the ATCC under accession number 98600;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cc162_1 deposited with the ATCC under accession number 98600;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cc162_1 deposited with the ATCC under accession number 98600;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cc162_1 deposited with the ATCC under accession number 98600;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:28;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 156 to nucleotide 413; the nucleotide sequence of SEQ ID NO:27 from nucleotide 198 to nucleotide 413; the nucleotide sequence of the full-length protein coding sequence of clone cc162_1 deposited with the ATCC under accession number 98600; or the nucleotide sequence of a mature protein coding sequence of clone cc162_1 deposited with the ATCC under accession number 98600. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cc162_1 deposited with the ATCC under accession number 98600. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28 from amino acid 1 to amino acid 66. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:28.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:27.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 25 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:27, but excluding the poly(A) tail at the
 - 30 3' end of SEQ ID NO:27; and
 - (ab) the nucleotide sequence of the cDNA insert of clone cc162_1 deposited with the ATCC under accession number 98600; and

- (ii) hybridizing said probe(s) to human DNA; and
- (iii) isolating the DNA polynucleotide detected with the probe(s);

and

5 (b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(bb) the nucleotide sequence of the cDNA insert of clone cc162_1 deposited with the ATCC under accession number 98600; and

15 (ii) hybridizing said primer(s) to human DNA;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:27 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 156 to nucleotide 413, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 156 to nucleotide 413, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 156 to nucleotide 413. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 198 to nucleotide 413, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 198 to nucleotide 413, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 198 to nucleotide 413.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;
- 5 (b) the amino acid sequence of SEQ ID NO:28 from amino acid 1 to amino acid 66;
- (c) fragments of the amino acid sequence of SEQ ID NO:28 comprising eight consecutive amino acids of SEQ ID NO:28; and
- (d) the amino acid sequence encoded by the cDNA insert of clone
10 cc162_1 deposited with the ATCC under accession number 98600;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28 or the amino acid sequence of SEQ ID NO:28 from amino acid 1 to amino acid 66. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid
15 sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:28, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:28.

20 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:29 from nucleotide 180 to nucleotide 737;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 240 to nucleotide 737;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone if87_1 deposited with the ATCC under
30 accession number 98600;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone if87_1 deposited with the ATCC under accession number 98600;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone if87_1 deposited with the ATCC under accession number 98600;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone if87_1 deposited with the ATCC under accession number 98600;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:30;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 180 to nucleotide 737; the nucleotide sequence of SEQ ID NO:29 from nucleotide 240 to nucleotide 737; the nucleotide sequence of the full-length protein coding sequence of clone if87_1 deposited with the ATCC under accession number 98600; or the nucleotide sequence of a mature protein coding sequence of clone if87_1 deposited with the ATCC under accession number 98600. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone if87_1 deposited with the ATCC under accession number 98600. In yet other
20 preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30 from amino acid 1 to amino acid 88. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more
25 preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 88 to amino acid 97 of SEQ ID NO:30.
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Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:29.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:29, but excluding the poly(A) tail at the
 - 10 3' end of SEQ ID NO:29; and
 - (ab) the nucleotide sequence of the cDNA insert of clone if87_1 deposited with the ATCC under accession number 98600; and
 - (ii) hybridizing said probe(s) to human DNA; and
 - 15 (iii) isolating the DNA polynucleotide detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that
 - 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:29, but excluding the poly(A) tail at the
 - 3' end of SEQ ID NO:29; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
 - 25 if87_1 deposited with the ATCC under accession number 98600; and
 - (ii) hybridizing said primer(s) to human DNA;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide product of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29, but

excluding the poly(A) tail at the 3' end of SEQ ID NO:29. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 180 to nucleotide 737, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 180 to nucleotide 737, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 180 to nucleotide 737. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 240 to nucleotide 737, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 240 to nucleotide 737, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 240 to nucleotide 737.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;
- (b) the amino acid sequence of SEQ ID NO:30 from amino acid 1 to amino acid 88;
- (c) fragments of the amino acid sequence of SEQ ID NO:30 comprising eight consecutive amino acids of SEQ ID NO:30; and
- (d) the amino acid sequence encoded by the cDNA insert of clone if87_1 deposited with the ATCC under accession number 98600;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:30 or the amino acid sequence of SEQ ID NO:30 from amino acid 1 to amino acid 88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:30, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 88 to amino acid 97 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 2294 to nucleotide 2845;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 2387 to nucleotide 2845;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone nn103_4 deposited with the ATCC under accession number 98600;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone nn103_4 deposited with the ATCC under accession number 98600;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone nn103_4 deposited with the ATCC under accession number 98600;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone nn103_4 deposited with the ATCC under accession number 98600;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:32;
- 20 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:32;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 25 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:31 from nucleotide 2294 to nucleotide 2845; the nucleotide sequence of SEQ ID NO:31 from nucleotide 2387 to nucleotide 2845; the nucleotide sequence of the full-length protein coding sequence of clone nn103_4 deposited with the ATCC under accession number 98600; or the nucleotide sequence of a mature protein coding sequence of clone

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nn103_4 deposited with the ATCC under accession number 98600. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone nn103_4 deposited with the ATCC under accession number 98600. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:32 from amino acid 12 to amino acid 137. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:32, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 87 to amino acid 96 of SEQ ID NO:32.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:31.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and
 - (ab) the nucleotide sequence of the cDNA insert of clone nn103_4 deposited with the ATCC under accession number 98600; and
 - (ii) hybridizing said probe(s) to human DNA; and
 - (iii) isolating the DNA polynucleotide detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and
- (bb) the nucleotide sequence of the cDNA insert of clone nn103_4 deposited with the ATCC under accession number 98600; and
- 10 (ii) hybridizing said primer(s) to human DNA;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:31 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 2294 to nucleotide 2845, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 2294 to nucleotide 2845, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 2294 to nucleotide 2845. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 2387 to nucleotide 2845, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 2387 to nucleotide 2845, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 2387 to nucleotide 2845.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:32;

(b) the amino acid sequence of SEQ ID NO:32 from amino acid 12 to amino acid 137;

(c) fragments of the amino acid sequence of SEQ ID NO:32 comprising eight consecutive amino acids of SEQ ID NO:32; and

5 (d) the amino acid sequence encoded by the cDNA insert of clone nn103_4 deposited with the ATCC under accession number 98600;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:32 or the amino acid sequence of SEQ ID NO:32 from amino acid 12 to amino acid 137. In further preferred
10 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:32, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid
15 sequence from amino acid 87 to amino acid 96 of SEQ ID NO:32.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33;

20 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 1280 to nucleotide 1504;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone np206_8 deposited with the ATCC under accession number 98600;

25 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone np206_8 deposited with the ATCC under accession number 98600;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone np206_8 deposited with the ATCC under
30 accession number 98600;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone np206_8 deposited with the ATCC under accession number 98600;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:34;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:34;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:33 from nucleotide 1280 to nucleotide 1504; the nucleotide sequence of the full-length protein coding sequence of clone np206_8 deposited with the ATCC under accession number 98600; or the nucleotide sequence of a mature protein coding sequence of clone np206_8 deposited with the ATCC under accession number 98600. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone np206_8 deposited with the ATCC under accession number 98600. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:34 from amino acid 1 to amino acid 26. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:34, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:34.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:33.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(ab) the nucleotide sequence of the cDNA insert of clone np206_8 deposited with the ATCC under accession number 98600; and

(ii) hybridizing said probe(s) to human DNA; and

(iii) isolating the DNA polynucleotide detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(bb) the nucleotide sequence of the cDNA insert of clone np206_8 deposited with the ATCC under accession number 98600; and

(ii) hybridizing said primer(s) to human DNA;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:33 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 1280 to nucleotide 1504, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 1280 to nucleotide 1504,

to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 1280 to nucleotide 1504.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the
5 group consisting of:

- (a) the amino acid sequence of SEQ ID NO:34;
- (b) the amino acid sequence of SEQ ID NO:34 from amino acid 1 to amino acid 26;
- (c) fragments of the amino acid sequence of SEQ ID NO:34 comprising
10 eight consecutive amino acids of SEQ ID NO:34; and
- (d) the amino acid sequence encoded by the cDNA insert of clone np206_8 deposited with the ATCC under accession number 98600;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:34 or the amino acid sequence
15 of SEQ ID NO:34 from amino acid 1 to amino acid 26. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:34, or a protein comprising a fragment of the amino acid sequence of SEQ ID
20 NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:34.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:35;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 133 to nucleotide 432;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone nt746_4 deposited with the ATCC under
30 accession number 98600;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone nt746_4 deposited with the ATCC under accession number 98600;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone nt746_4 deposited with the ATCC under accession number 98600;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone nt746_4 deposited with the ATCC under accession number 98600;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:36;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:35 from nucleotide 133 to nucleotide 432; the nucleotide sequence of the full-length protein coding sequence of clone nt746_4 deposited with the ATCC under accession number 98600; or the nucleotide sequence of a mature protein coding sequence of clone nt746_4 deposited with the ATCC under accession number 98600. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone nt746_4 deposited with the ATCC under accession number 98600. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36 from amino acid 1 to amino acid 70. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:36, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:36.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:35.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:35, but excluding the poly(A) tail at the
- 10 3' end of SEQ ID NO:35; and
- (ab) the nucleotide sequence of the cDNA insert of clone nt746_4 deposited with the ATCC under accession number 98600; and
- (ii) hybridizing said probe(s) to human DNA; and
- 15 (iii) isolating the DNA polynucleotide detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 nt746_4 deposited with the ATCC under accession number 98600; and
- (ii) hybridizing said primer(s) to human DNA;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide product of step (b)(iii).

- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:35 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:35 , but

excluding the poly(A) tail at the 3' end of SEQ ID NO:35. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 133 to nucleotide 432, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 133 to nucleotide 432, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 133 to nucleotide 432.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:36;
- (b) the amino acid sequence of SEQ ID NO:36 from amino acid 1 to amino acid 70;
- (c) fragments of the amino acid sequence of SEQ ID NO:36 comprising eight consecutive amino acids of SEQ ID NO:36; and
- (d) the amino acid sequence encoded by the cDNA insert of clone nt746_4 deposited with the ATCC under accession number 98600;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:36 or the amino acid sequence of SEQ ID NO:36 from amino acid 1 to amino acid 70. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:36, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:36.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 31 to nucleotide 201;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pe286_1 deposited with the ATCC under accession number 98600;

5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pe286_1 deposited with the ATCC under accession number 98600;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pe286_1 deposited with the ATCC under accession number 98600;

10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pe286_1 deposited with the ATCC under accession number 98600;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:38;

15 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:38;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

20 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:37 from nucleotide 31 to nucleotide 201; the nucleotide sequence of the full-length protein coding sequence of clone pe286_1 deposited with the ATCC under accession number 98600; or the nucleotide sequence of a mature protein coding sequence of clone pe286_1 deposited with the ATCC under accession number 98600. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pe286_1 deposited with the ATCC under accession number 98600. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:38 from amino acid 1 to amino acid 49. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:38, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment
5 comprising the amino acid sequence from amino acid 23 to amino acid 32 of SEQ ID NO:38.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:37.

Further embodiments of the invention provide isolated polynucleotides produced
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(ab) the nucleotide sequence of the cDNA insert of clone pe286_1 deposited with the ATCC under accession number 98600; and

20 (ii) hybridizing said probe(s) to human DNA; and

(iii) isolating the DNA polynucleotide detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

30 (bb) the nucleotide sequence of the cDNA insert of clone pe286_1 deposited with the ATCC under accession number 98600; and

(ii) hybridizing said primer(s) to human DNA;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:37 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 31 to nucleotide
10 201, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 31 to nucleotide 201, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 31 to nucleotide 201.

In other embodiments, the present invention provides a composition comprising
15 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:38;
- (b) the amino acid sequence of SEQ ID NO:38 from amino acid 1 to amino acid 49;
- 20 (c) fragments of the amino acid sequence of SEQ ID NO:38 comprising eight consecutive amino acids of SEQ ID NO:38; and
- (d) the amino acid sequence encoded by the cDNA insert of clone pe286_1 deposited with the ATCC under accession number 98600;

the protein being substantially free from other mammalian proteins. Preferably such
25 protein comprises the amino acid sequence of SEQ ID NO:38 or the amino acid sequence of SEQ ID NO:38 from amino acid 1 to amino acid 49. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ
30 ID NO:38, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 23 to amino acid 32 of SEQ ID NO:38.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 843 to nucleotide 1004;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb7_1 deposited with the ATCC under accession number 98600;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb7_1 deposited with the ATCC under accession number 98600;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb7_1 deposited with the ATCC under accession
15 number 98600;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb7_1 deposited with the ATCC under accession number 98600;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- 20 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:40;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 25 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
30 NO:39 from nucleotide 843 to nucleotide 1004; the nucleotide sequence of the full-length protein coding sequence of clone yb7_1 deposited with the ATCC under accession number 98600; or the nucleotide sequence of a mature protein coding sequence of clone yb7_1 deposited with the ATCC under accession number 98600. In other preferred

embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb7_1 deposited with the ATCC under accession number 98600.

In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40
5 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:40.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:39.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

20 (ab) the nucleotide sequence of the cDNA insert of clone yb7_1 deposited with the ATCC under accession number 98600; and

(ii) hybridizing said probe(s) to human DNA; and

25 (iii) isolating the DNA polynucleotide detected with the probe(s);

and

(b) a process comprising the steps of:

30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

(bb) the nucleotide sequence of the cDNA insert of clone yb7_1 deposited with the ATCC under accession number 98600; and

- (ii) hybridizing said primer(s) to human DNA;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide product of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
10 ID NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 843 to nucleotide 1004, and extending contiguously from a nucleotide sequence corresponding to the 5' end
15 of said sequence of SEQ ID NO:39 from nucleotide 843 to nucleotide 1004, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 843 to nucleotide 1004.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the
20 group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;
- (b) fragments of the amino acid sequence of SEQ ID NO:40 comprising eight consecutive amino acids of SEQ ID NO:40; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
25 yb7_1 deposited with the ATCC under accession number 98600;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:40. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably
30 comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:40.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 179 to nucleotide 4285;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone am728_60 deposited with the ATCC under accession number 98621;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone am728_60 deposited with the ATCC under accession number 98621;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone am728_60 deposited with the ATCC under
15 accession number 98621;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone am728_60 deposited with the ATCC under accession number 98621;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
- 20 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:42;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 25 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
30 NO:41 from nucleotide 179 to nucleotide 4285; the nucleotide sequence of the full-length protein coding sequence of clone am728_60 deposited with the ATCC under accession number 98621; or the nucleotide sequence of a mature protein coding sequence of clone am728_60 deposited with the ATCC under accession number 98621. In other preferred

embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone am728_60 deposited with the ATCC under accession number 98621. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 679 to amino acid 688 of SEQ ID NO:42.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:41.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:
15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:41; and
(ab) the nucleotide sequence of the cDNA insert of clone
20 am728_60 deposited with the ATCC under accession number 98621;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the
25 probe(s);

and

(b) a process comprising the steps of:
(i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
30 the group consisting of:

(ba) SEQ ID NO:41; and

(bb) the nucleotide sequence of the cDNA insert of clone am728_60 deposited with the ATCC under accession number 98621;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and
10 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 179 to nucleotide 4285, and extending contiguously from a nucleotide
15 sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 179 to nucleotide 4285, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 179 to nucleotide 4285.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the
20 group consisting of:

(a) the amino acid sequence of SEQ ID NO:42;

(b) fragments of the amino acid sequence of SEQ ID NO:42, each fragment comprising eight consecutive amino acids of SEQ ID NO:42; and

(c) the amino acid sequence encoded by the cDNA insert of clone
25 am728_60 deposited with the ATCC under accession number 98621;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably
30 comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:42, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 679 to amino acid 688 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 108 to nucleotide 254;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 225 to nucleotide 254;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bf377_1 deposited with the ATCC under
10 accession number 98621;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bf377_1 deposited with the ATCC under accession number 98621;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bf377_1 deposited with the ATCC under accession number 98621;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bf377_1 deposited with the ATCC under accession number 98621;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:44;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:44;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide that hybridizes under stringent conditions to any
30 one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:43 from nucleotide 108 to nucleotide 254; the nucleotide sequence of SEQ ID NO:43 from nucleotide 225 to nucleotide 254; the nucleotide sequence of the full-length protein

coding sequence of clone bf377_1 deposited with the ATCC under accession number 98621; or the nucleotide sequence of a mature protein coding sequence of clone bf377_1 deposited with the ATCC under accession number 98621. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bf377_1 deposited with the ATCC under accession number 98621. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:44, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 19 to amino acid 28 of SEQ ID NO:44.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:43.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(ab) the nucleotide sequence of the cDNA insert of clone bf377_1 deposited with the ATCC under accession number 98621;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(bb) the nucleotide sequence of the cDNA insert of clone bf377_1 deposited with the ATCC under accession number 98621;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 108 to nucleotide 254, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 108 to nucleotide 254, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 108 to nucleotide 254. Also preferably the polynucleotide isolated according to the above
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 225 to nucleotide 254, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 225 to nucleotide 254, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 225 to nucleotide 254.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:44;

(b) fragments of the amino acid sequence of SEQ ID NO:44, each
30 fragment comprising eight consecutive amino acids of SEQ ID NO:44; and

(c) the amino acid sequence encoded by the cDNA insert of clone bf377_1 deposited with the ATCC under accession number 98621;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably
5 comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:44, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 19 to amino acid 28 of SEQ ID NO:44.

In one embodiment, the present invention provides a composition comprising an
10 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 426 to nucleotide 569;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 546 to nucleotide 569;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw354_1 deposited with the ATCC under accession number 98621;
- 20 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw354_1 deposited with the ATCC under accession number 98621;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw354_1 deposited with the ATCC under
25 accession number 98621;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw354_1 deposited with the ATCC under accession number 98621;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:46;
- 30 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:46;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:45 from nucleotide 426 to nucleotide 569; the nucleotide sequence of SEQ ID NO:45 from nucleotide 546 to nucleotide 569; the nucleotide sequence of the full-length protein
10 coding sequence of clone cw354_1 deposited with the ATCC under accession number 98621; or the nucleotide sequence of a mature protein coding sequence of clone cw354_1 deposited with the ATCC under accession number 98621. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw354_1 deposited with the ATCC under accession number
15 98621. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:46, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence
20 of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 19 to amino acid 28 of SEQ ID NO:46.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:45.

Further embodiments of the invention provide isolated polynucleotides produced
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

(ab) the nucleotide sequence of the cDNA insert of clone cw354_1 deposited with the ATCC under accession number 98621;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

(bb) the nucleotide sequence of the cDNA insert of clone cw354_1 deposited with the ATCC under accession number 98621;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

15 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45, and
20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:45 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 426 to nucleotide
25 569, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 426 to nucleotide 569, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 426 to nucleotide 569. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
30 NO:45 from nucleotide 546 to nucleotide 569, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 546 to nucleotide 569, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 546 to nucleotide 569.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:46;
- 5 (b) fragments of the amino acid sequence of SEQ ID NO:46, each fragment comprising eight consecutive amino acids of SEQ ID NO:46; and
- (c) the amino acid sequence encoded by the cDNA insert of clone cw354_1 deposited with the ATCC under accession number 98621;

the protein being substantially free from other mammalian proteins. Preferably such
10 protein comprises the amino acid sequence of SEQ ID NO:46. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino
15 acids of SEQ ID NO:46, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 19 to amino acid 28 of SEQ ID NO:46.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
20 NO:47;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 151 to nucleotide 891;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 595 to nucleotide 891;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone nm134_4 deposited with the ATCC under accession number 98621;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone nm134_4 deposited with the ATCC under accession number
30 98621;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone nm134_4 deposited with the ATCC under accession number 98621;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone nm134_4 deposited with the ATCC under accession number 98621;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;

5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:48;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
15 NO:47 from nucleotide 151 to nucleotide 891; the nucleotide sequence of SEQ ID NO:47 from nucleotide 595 to nucleotide 891; the nucleotide sequence of the full-length protein coding sequence of clone nm134_4 deposited with the ATCC under accession number 98621; or the nucleotide sequence of a mature protein coding sequence of clone nm134_4 deposited with the ATCC under accession number 98621. In other preferred
20 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone nm134_4 deposited with the ATCC under accession number 98621. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48 from amino acid 104 to amino acid 163. In further preferred embodiments, the present
25 invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:48, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment
30 comprising the amino acid sequence from amino acid 118 to amino acid 127 of SEQ ID NO:48.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:47.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

5 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

10 (ab) the nucleotide sequence of the cDNA insert of clone nm134_4 deposited with the ATCC under accession number 98621;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

15 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (ba) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

(bb) the nucleotide sequence of the cDNA insert of clone nm134_4 deposited with the ATCC under accession number 98621;

25 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and
30 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 151 to nucleotide 891, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 151 to nucleotide 891, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 151 to nucleotide 891. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 595 to nucleotide 891, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 595 to nucleotide 891, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 595 to nucleotide 891.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
- (b) the amino acid sequence of SEQ ID NO:48 from amino acid 104 to amino acid 163;
- (c) fragments of the amino acid sequence of SEQ ID NO:48, each fragment comprising eight consecutive amino acids of SEQ ID NO:48; and
- (d) the amino acid sequence encoded by the cDNA insert of clone nm134_4 deposited with the ATCC under accession number 98621;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48 or the amino acid sequence of SEQ ID NO:48 from amino acid 104 to amino acid 163. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 118 to amino acid 127 of SEQ ID NO:48.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 1909 to nucleotide 2127;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 2074 to nucleotide 2127;

5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb11_1 deposited with the ATCC under accession number 98621;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb11_1 deposited with the ATCC under accession number
10 98621;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb11_1 deposited with the ATCC under accession number 98621;

(g) a polynucleotide encoding a mature protein encoded by the cDNA
15 insert of clone yb11_1 deposited with the ATCC under accession number 98621;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:50;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment
20 comprising eight consecutive amino acids of SEQ ID NO:50;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:49 from nucleotide 1909 to nucleotide 2127; the nucleotide sequence of SEQ ID NO:49 from nucleotide 2074 to nucleotide 2127; the nucleotide sequence of the full-length
30 protein coding sequence of clone yb11_1 deposited with the ATCC under accession number 98621; or the nucleotide sequence of a mature protein coding sequence of clone yb11_1 deposited with the ATCC under accession number 98621. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by

the cDNA insert of clone yb11_1 deposited with the ATCC under accession number 98621. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more
5 preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:50, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 31 to amino acid 40 of SEQ ID NO:50.

Other embodiments provide the gene corresponding to the cDNA sequence of
10 SEQ ID NO:49.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
15 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
20 yb11_1 deposited with the ATCC under accession number 98621;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 25 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 30 (ba) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and
 - (bb) the nucleotide sequence of the cDNA insert of clone yb11_1 deposited with the ATCC under accession number 98621;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:49 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the
10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 1909 to nucleotide 2127, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 1909 to nucleotide 2127, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49
15 from nucleotide 1909 to nucleotide 2127. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 2074 to nucleotide 2127, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 2074 to nucleotide 2127, to a nucleotide sequence
20 corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 2074 to nucleotide 2127.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 25 (a) the amino acid sequence of SEQ ID NO:50;
(b) fragments of the amino acid sequence of SEQ ID NO:50, each fragment comprising eight consecutive amino acids of SEQ ID NO:50; and
(c) the amino acid sequence encoded by the cDNA insert of clone yb11_1 deposited with the ATCC under accession number 98621;

30 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:50. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:50, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 31 to amino acid 40 of SEQ ID NO:50.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:51 from nucleotide 1077 to nucleotide 1733;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 1158 to nucleotide 1733;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yc2_1 deposited with the ATCC under
15 accession number 98621;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yc2_1 deposited with the ATCC under accession number 98621;
- (f) a polynucleotide comprising the nucleotide sequence of a mature
20 protein coding sequence of clone yc2_1 deposited with the ATCC under accession number 98621;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yc2_1 deposited with the ATCC under accession number 98621;
- (h) a polynucleotide encoding a protein comprising the amino acid
25 sequence of SEQ ID NO:52;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:52;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of
30 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:51 from nucleotide 1077 to nucleotide 1733; the nucleotide sequence of SEQ ID NO:51 from nucleotide 1158 to nucleotide 1733; the nucleotide sequence of the full-length protein coding sequence of clone yc2_1 deposited with the ATCC under accession number 98621; or the nucleotide sequence of a mature protein coding sequence of clone yc2_1 deposited with the ATCC under accession number 98621. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yc2_1 deposited with the ATCC under accession number 98621.

In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:52, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 104 to amino acid 113 of SEQ ID NO:52.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:51.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and

(ab) the nucleotide sequence of the cDNA insert of clone yc2_1 deposited with the ATCC under accession number 98621;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and

(bb) the nucleotide sequence of the cDNA insert of clone yc2_1 deposited with the ATCC under accession number 98621;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:51 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 1077 to nucleotide 1733, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 1077 to nucleotide 1733, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 1077 to nucleotide 1733. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 1158 to nucleotide 1733, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 1158 to nucleotide 1733, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 1158 to nucleotide 1733.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:52;
- (b) fragments of the amino acid sequence of SEQ ID NO:52, each fragment comprising eight consecutive amino acids of SEQ ID NO:52; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
5 yc2_1 deposited with the ATCC under accession number 98621;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:52. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably
10 comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:52, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 104 to amino acid 113 of SEQ ID NO:52.

In one embodiment, the present invention provides a composition comprising an
15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 257 to nucleotide 622;
- 20 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ff168_12 deposited with the ATCC under accession number 98623;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ff168_12 deposited with the ATCC under accession number
25 98623;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ff168_12 deposited with the ATCC under accession number 98623;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA
30 insert of clone ff168_12 deposited with the ATCC under accession number 98623;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:54;

5 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:53 from nucleotide 257 to nucleotide 622; the nucleotide sequence of the full-length protein coding sequence of clone ff168_12 deposited with the ATCC under accession number 98623; or the nucleotide sequence of a mature protein coding sequence of clone ff168_12 deposited with the ATCC under accession number 98623. In other preferred
15 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ff168_12 deposited with the ATCC under accession number 98623. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more
20 preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 56 to amino acid 65 of SEQ ID NO:54.

Other embodiments provide the gene corresponding to the cDNA sequence of
25 SEQ ID NO:53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
- 30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:53; but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

- (ab) the nucleotide sequence of the cDNA insert of clone ff168_12 deposited with the ATCC under accession number 98623;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 ff168_12 deposited with the ATCC under accession number 98623;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 257 to nucleotide 622, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 257 to nucleotide 622, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide
- 30 257 to nucleotide 622.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:54;
- (b) fragments of the amino acid sequence of SEQ ID NO:54, each fragment comprising eight consecutive amino acids of SEQ ID NO:54; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ff168_12 deposited with the ATCC under accession number 98623;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:54. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably
- 10 comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 56 to amino acid 65 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an

15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 1323 to nucleotide 1829;
- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 1539 to nucleotide 1829;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ls9_1 deposited with the ATCC under accession number 98623;
- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ls9_1 deposited with the ATCC under accession number 98623;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ls9_1 deposited with the ATCC under accession
- 30 number 98623;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ls9_1 deposited with the ATCC under accession number 98623;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:56;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:55 from nucleotide 1323 to nucleotide 1829; the nucleotide sequence of SEQ ID NO:55 from nucleotide 1539 to nucleotide 1829; the nucleotide sequence of the full-length protein coding sequence of clone ls9_1 deposited with the ATCC under accession number 98623; or the nucleotide sequence of a mature protein coding sequence of clone ls9_1 deposited with the ATCC under accession number 98623. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ls9_1 deposited with the ATCC under accession number 98623.

In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 79 to amino acid 88 of SEQ ID NO:56.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:55.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

(ab) the nucleotide sequence of the cDNA insert of clone ls9_1 deposited with the ATCC under accession number 98623;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

20 (bb) the nucleotide sequence of the cDNA insert of clone ls9_1 deposited with the ATCC under accession number 98623;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55. Also preferably the
30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 1323 to nucleotide 1829, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 1323 to nucleotide 1829,

to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 1323 to nucleotide 1829. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 1539 to nucleotide 1829, and extending
5 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 1539 to nucleotide 1829, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 1539 to nucleotide 1829.

In other embodiments, the present invention provides a composition comprising
10 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:56;
- (b) fragments of the amino acid sequence of SEQ ID NO:56, each fragment comprising eight consecutive amino acids of SEQ ID NO:56; and
15 (c) the amino acid sequence encoded by the cDNA insert of clone ls9_1 deposited with the ATCC under accession number 98623;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred
20 amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:56, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 79 to amino acid 88 of SEQ ID NO:56.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:57 from nucleotide 507 to nucleotide 722;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 615 to nucleotide 722;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone na1010_1 deposited with the ATCC under accession number 98623;

5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone na1010_1 deposited with the ATCC under accession number 98623;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone na1010_1 deposited with the ATCC under accession number 98623;

10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone na1010_1 deposited with the ATCC under accession number 98623;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:58;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:58;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:57 from nucleotide 507 to nucleotide 722; the nucleotide sequence of SEQ ID NO:57
25 from nucleotide 615 to nucleotide 722; the nucleotide sequence of the full-length protein coding sequence of clone na1010_1 deposited with the ATCC under accession number 98623; or the nucleotide sequence of a mature protein coding sequence of clone na1010_1 deposited with the ATCC under accession number 98623. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by
30 the cDNA insert of clone na1010_1 deposited with the ATCC under accession number 98623. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more

preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:58, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 31 to amino acid 40 of SEQ ID NO:58.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:57.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and
 - 15 (ab) the nucleotide sequence of the cDNA insert of clone na1010_1 deposited with the ATCC under accession number 98623;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 20 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (ba) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and
 - (bb) the nucleotide sequence of the cDNA insert of clone na1010_1 deposited with the ATCC under accession number 98623;
 - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:57 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 507 to nucleotide 722, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 507 to nucleotide 722, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 507 to nucleotide 722. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 615 to nucleotide 722, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from
15 nucleotide 615 to nucleotide 722, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 615 to nucleotide 722.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:58;
- (b) fragments of the amino acid sequence of SEQ ID NO:58, each fragment comprising eight consecutive amino acids of SEQ ID NO:58; and
- (c) the amino acid sequence encoded by the cDNA insert of clone na1010_1 deposited with the ATCC under accession number 98623;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:58. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino
30 acids of SEQ ID NO:58, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 31 to amino acid 40 of SEQ ID NO:58.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 673 to nucleotide 987;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 868 to nucleotide 987;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone nf87_1 deposited with the ATCC under accession number 98623;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone nf87_1 deposited with the ATCC under accession number 98623;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone nf87_1 deposited with the ATCC under accession number 98623;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone nf87_1 deposited with the ATCC under accession number 98623;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:60;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:60;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:59 from nucleotide 673 to nucleotide 987; the nucleotide sequence of SEQ ID NO:59 from nucleotide 868 to nucleotide 987; the nucleotide sequence of the full-length protein

coding sequence of clone nf87_1 deposited with the ATCC under accession number 98623; or the nucleotide sequence of a mature protein coding sequence of clone nf87_1 deposited with the ATCC under accession number 98623. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert
5 of clone nf87_1 deposited with the ATCC under accession number 98623. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:60, or a polynucleotide
10 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:60.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:59.

15 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
20 consisting of:

- (aa) SEQ ID NO:59, but excluding the poly(A) tail at the
3' end of SEQ ID NO:59; and

- (ab) the nucleotide sequence of the cDNA insert of clone
nf87_1 deposited with the ATCC under accession number 98623;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the
probe(s);

and

30 (b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and

(bb) the nucleotide sequence of the cDNA insert of clone nf87_1 deposited with the ATCC under accession number 98623;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:59 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 673 to nucleotide 987, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 673 to nucleotide 987, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide 673 to nucleotide 987. Also preferably the polynucleotide isolated according to the above
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 868 to nucleotide 987, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 868 to nucleotide 987, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide 868 to nucleotide 987.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:60;

(b) fragments of the amino acid sequence of SEQ ID NO:60, each
30 fragment comprising eight consecutive amino acids of SEQ ID NO:60; and

(c) the amino acid sequence encoded by the cDNA insert of clone nf87_1 deposited with the ATCC under accession number 98623;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:60. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:60, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:60.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 57 to nucleotide 824;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 114 to nucleotide 824;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone nh796_1 deposited with the ATCC under accession number 98623;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone nh796_1 deposited with the ATCC under accession number 98623;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone nh796_1 deposited with the ATCC under accession number 98623;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone nh796_1 deposited with the ATCC under accession number 98623;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:62;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:62;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:61 from nucleotide 57 to nucleotide 824; the nucleotide sequence of SEQ ID NO:61 from nucleotide 114 to nucleotide 824; the nucleotide sequence of the full-length protein
10 coding sequence of clone nh796_1 deposited with the ATCC under accession number 98623; or the nucleotide sequence of a mature protein coding sequence of clone nh796_1 deposited with the ATCC under accession number 98623. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone nh796_1 deposited with the ATCC under accession number
15 98623. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:62, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence
20 of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 123 to amino acid 132 of SEQ ID NO:62.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:61.

Further embodiments of the invention provide isolated polynucleotides produced
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(ab) the nucleotide sequence of the cDNA insert of clone nh796_1 deposited with the ATCC under accession number 98623;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(bb) the nucleotide sequence of the cDNA insert of clone nh796_1 deposited with the ATCC under accession number 98623;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61, and
20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:61 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 57 to nucleotide
25 824, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 57 to nucleotide 824, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 57 to nucleotide 824. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
30 NO:61 from nucleotide 114 to nucleotide 824, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 114 to nucleotide 824, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 114 to nucleotide 824.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:62;
 - 5 (b) fragments of the amino acid sequence of SEQ ID NO:62, each fragment comprising eight consecutive amino acids of SEQ ID NO:62; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone nh796_1 deposited with the ATCC under accession number 98623;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:62. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino
- 15 acids of SEQ ID NO:62, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 123 to amino acid 132 of SEQ ID NO:62.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:63;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 297 to nucleotide 542;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 510 to nucleotide 542;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone nn229_1 deposited with the ATCC under accession number 98623;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone nn229_1 deposited with the ATCC under accession number
- 30 98623;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone nn229_1 deposited with the ATCC under accession number 98623;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone nn229_1 deposited with the ATCC under accession number 98623;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:64;

5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:64;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
15 NO:63 from nucleotide 297 to nucleotide 542; the nucleotide sequence of SEQ ID NO:63 from nucleotide 510 to nucleotide 542; the nucleotide sequence of the full-length protein coding sequence of clone nn229_1 deposited with the ATCC under accession number 98623; or the nucleotide sequence of a mature protein coding sequence of clone nn229_1 deposited with the ATCC under accession number 98623. In other preferred
20 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone nn229_1 deposited with the ATCC under accession number 98623. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more
25 preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:64, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID NO:64.

Other embodiments provide the gene corresponding to the cDNA sequence of
30 SEQ ID NO:63.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

(ab) the nucleotide sequence of the cDNA insert of clone nn229_1 deposited with the ATCC under accession number 98623;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

20 (bb) the nucleotide sequence of the cDNA insert of clone nn229_1 deposited with the ATCC under accession number 98623;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:63 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63. Also preferably the
30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 297 to nucleotide 542, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 297 to nucleotide 542, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 297 to nucleotide 542. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 510 to nucleotide 542, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 510 to nucleotide 542, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 510 to nucleotide 542.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:64;
- (b) fragments of the amino acid sequence of SEQ ID NO:64, each fragment comprising eight consecutive amino acids of SEQ ID NO:64; and
- (c) the amino acid sequence encoded by the cDNA insert of clone nn229_1 deposited with the ATCC under accession number 98623;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:64. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:64, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID NO:64.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 547 to nucleotide 750;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 601 to nucleotide 750;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone np156_1 deposited with the ATCC under accession number 98623;

5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone np156_1 deposited with the ATCC under accession number 98623;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone np156_1 deposited with the ATCC under accession number 98623;

10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone np156_1 deposited with the ATCC under accession number 98623;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:66;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:66;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:65 from nucleotide 547 to nucleotide 750; the nucleotide sequence of SEQ ID NO:65
25 from nucleotide 601 to nucleotide 750; the nucleotide sequence of the full-length protein coding sequence of clone np156_1 deposited with the ATCC under accession number 98623; or the nucleotide sequence of a mature protein coding sequence of clone np156_1 deposited with the ATCC under accession number 98623. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by
30 the cDNA insert of clone np156_1 deposited with the ATCC under accession number 98623. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more

preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:66, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 29 to amino acid 38 of SEQ ID NO:66.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:65.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:
10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65; and

15 (ab) the nucleotide sequence of the cDNA insert of clone np156_1 deposited with the ATCC under accession number 98623;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

20 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:
25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65; and

(bb) the nucleotide sequence of the cDNA insert of clone np156_1 deposited with the ATCC under accession number 98623;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:65 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:65, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:65. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 547 to nucleotide 750, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 547 to nucleotide 750, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide 547 to nucleotide 750. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 601 to nucleotide 750, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from
15 nucleotide 601 to nucleotide 750, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide 601 to nucleotide 750.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:66;
(b) fragments of the amino acid sequence of SEQ ID NO:66, each fragment comprising eight consecutive amino acids of SEQ ID NO:66; and
(c) the amino acid sequence encoded by the cDNA insert of clone np156_1 deposited with the ATCC under accession number 98623;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:66. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino
30 acids of SEQ ID NO:66, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 29 to amino acid 38 of SEQ ID NO:66.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 310 to nucleotide 459;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 445 to nucleotide 459;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bg570_1 deposited with the ATCC under accession number 98629;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bg570_1 deposited with the ATCC under accession number 98629;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bg570_1 deposited with the ATCC under accession number 98629;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bg570_1 deposited with the ATCC under accession number 98629;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:68;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:68;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:67 from nucleotide 310 to nucleotide 459; the nucleotide sequence of SEQ ID NO:67 from nucleotide 445 to nucleotide 459; the nucleotide sequence of the full-length protein

coding sequence of clone bg570_1 deposited with the ATCC under accession number 98629; or the nucleotide sequence of a mature protein coding sequence of clone bg570_1 deposited with the ATCC under accession number 98629. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bg570_1 deposited with the ATCC under accession number 98629. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:68, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 20 to amino acid 29 of SEQ ID NO:68.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:67.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and

(ab) the nucleotide sequence of the cDNA insert of clone bg570_1 deposited with the ATCC under accession number 98629;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and

(bb) the nucleotide sequence of the cDNA insert of clone bg570_1 deposited with the ATCC under accession number 98629;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:67 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 310 to nucleotide 459, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 310 to nucleotide 459, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 310 to nucleotide 459. Also preferably the polynucleotide isolated according to the above
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 445 to nucleotide 459, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 445 to nucleotide 459, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 445 to nucleotide 459.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:68;

(b) fragments of the amino acid sequence of SEQ ID NO:68, each
30 fragment comprising eight consecutive amino acids of SEQ ID NO:68; and

(c) the amino acid sequence encoded by the cDNA insert of clone bg570_1 deposited with the ATCC under accession number 98629;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:68. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:68, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 20 to amino acid 29 of SEQ ID NO:68.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 90 to nucleotide 1019;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 243 to nucleotide 1019;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bi120_2 deposited with the ATCC under accession number 98629;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bi120_2 deposited with the ATCC under accession number 98629;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bi120_2 deposited with the ATCC under accession number 98629;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bi120_2 deposited with the ATCC under accession number 98629;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:70;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:70;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:69 from nucleotide 90 to nucleotide 1019; the nucleotide sequence of SEQ ID NO:69 from nucleotide 243 to nucleotide 1019; the nucleotide sequence of the full-length protein
10 coding sequence of clone bi120_2 deposited with the ATCC under accession number 98629; or the nucleotide sequence of a mature protein coding sequence of clone bi120_2 deposited with the ATCC under accession number 98629. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bi120_2 deposited with the ATCC under accession number
15 98629. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:70, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence
20 of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 149 to amino acid 158 of SEQ ID NO:70.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:69.

Further embodiments of the invention provide isolated polynucleotides produced
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and

(ab) the nucleotide sequence of the cDNA insert of clone bi120_2 deposited with the ATCC under accession number 98629;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and

(bb) the nucleotide sequence of the cDNA insert of clone bi120_2 deposited with the ATCC under accession number 98629;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69, and
20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:69 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 90 to nucleotide
25 1019, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 90 to nucleotide 1019, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 90 to nucleotide 1019. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
30 NO:69 from nucleotide 243 to nucleotide 1019, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 243 to nucleotide 1019, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 243 to nucleotide 1019.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:70;
- 5 (b) fragments of the amino acid sequence of SEQ ID NO:70, each fragment comprising eight consecutive amino acids of SEQ ID NO:70; and
- (c) the amino acid sequence encoded by the cDNA insert of clone bi120_2 deposited with the ATCC under accession number 98629;

the protein being substantially free from other mammalian proteins. Preferably such
10 protein comprises the amino acid sequence of SEQ ID NO:70. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino
15 acids of SEQ ID NO:70, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 149 to amino acid 158 of SEQ ID NO:70.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
20 NO:71;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71 from nucleotide 682 to nucleotide 894;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bn594_1 deposited with the ATCC under
25 accession number 98629;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bn594_1 deposited with the ATCC under accession number 98629;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
30 protein coding sequence of clone bn594_1 deposited with the ATCC under accession number 98629;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bn594_1 deposited with the ATCC under accession number 98629;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:72;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:72;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:71 from nucleotide 682 to nucleotide 894; the nucleotide sequence of the full-length protein coding sequence of clone bn594_1 deposited with the ATCC under accession number 98629; or the nucleotide sequence of a mature protein coding sequence of clone bn594_1 deposited with the ATCC under accession number 98629. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bn594_1 deposited with the ATCC under accession number 98629. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:72, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 30 to amino acid 39 of SEQ ID NO:72.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:71.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

(ab) the nucleotide sequence of the cDNA insert of clone bn594_1 deposited with the ATCC under accession number 98629;

5 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

10 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (ba) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

(bb) the nucleotide sequence of the cDNA insert of clone bn594_1 deposited with the ATCC under accession number 98629;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

20 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:71 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71 from nucleotide 682 to nucleotide 894, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:71 from nucleotide 682 to nucleotide 894, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:71 from nucleotide 682 to nucleotide 894.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:72;
- 5 (b) fragments of the amino acid sequence of SEQ ID NO:72, each fragment comprising eight consecutive amino acids of SEQ ID NO:72; and
- (c) the amino acid sequence encoded by the cDNA insert of clone bn594_1 deposited with the ATCC under accession number 98629;

the protein being substantially free from other mammalian proteins. Preferably such
10 protein comprises the amino acid sequence of SEQ ID NO:72. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino
15 acids of SEQ ID NO:72, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 30 to amino acid 39 of SEQ ID NO:72.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
20 NO:73;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 1184 to nucleotide 1582;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 1265 to nucleotide 1582;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone en554_1 deposited with the ATCC under accession number 98629;
- (e) a polynucleotide encoding the full-length protein encoded by the
cDNA insert of clone en554_1 deposited with the ATCC under accession number
30 98629;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone en554_1 deposited with the ATCC under accession number 98629;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone en554_1 deposited with the ATCC under accession number 98629;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:74;

5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:74;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:73 from nucleotide 1184 to nucleotide 1582; the nucleotide sequence of SEQ ID NO:73 from nucleotide 1265 to nucleotide 1582; the nucleotide sequence of the full-length protein coding sequence of clone en554_1 deposited with the ATCC under accession number 98629; or the nucleotide sequence of a mature protein coding sequence of clone en554_1 deposited with the ATCC under accession number 98629. In other preferred
20 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone en554_1 deposited with the ATCC under accession number 98629. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more
25 preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:74, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:74.

Other embodiments provide the gene corresponding to the cDNA sequence of
30 SEQ ID NO:73.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

(ab) the nucleotide sequence of the cDNA insert of clone en554_1 deposited with the ATCC under accession number 98629;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

20 (bb) the nucleotide sequence of the cDNA insert of clone en554_1 deposited with the ATCC under accession number 98629;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:73 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73. Also preferably the
30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 1184 to nucleotide 1582, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 1184 to nucleotide 1582,

to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 1184 to nucleotide 1582. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 1265 to nucleotide 1582, and extending
5 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 1265 to nucleotide 1582, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 1265 to nucleotide 1582.

In other embodiments, the present invention provides a composition comprising
10 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:74;
- (b) fragments of the amino acid sequence of SEQ ID NO:74, each fragment comprising eight consecutive amino acids of SEQ ID NO:74; and
15 (c) the amino acid sequence encoded by the cDNA insert of clone en554_1 deposited with the ATCC under accession number 98629;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:74. In further preferred
20 amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:74, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:74.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:75 from nucleotide 79 to nucleotide 504;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 322 to nucleotide 504;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone na474_10 deposited with the ATCC under accession number 98629;

5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone na474_10 deposited with the ATCC under accession number 98629;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone na474_10 deposited with the ATCC under accession number 98629;

10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone na474_10 deposited with the ATCC under accession number 98629;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:76;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:76;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:75 from nucleotide 79 to nucleotide 504; the nucleotide sequence of SEQ ID NO:75
25 from nucleotide 322 to nucleotide 504; the nucleotide sequence of the full-length protein coding sequence of clone na474_10 deposited with the ATCC under accession number 98629; or the nucleotide sequence of a mature protein coding sequence of clone na474_10 deposited with the ATCC under accession number 98629. In other preferred
30 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone na474_10 deposited with the ATCC under accession number 98629. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more

preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:76, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 66 to amino acid 75 of SEQ ID NO:76.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:75.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and
 - 15 (ab) the nucleotide sequence of the cDNA insert of clone na474_10 deposited with the ATCC under accession number 98629;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
 - 20 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (ba) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and
 - (bb) the nucleotide sequence of the cDNA insert of clone na474_10 deposited with the ATCC under accession number 98629;
 - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:75 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:75, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:75. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 79 to nucleotide 504, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 79 to nucleotide 504, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 79 to nucleotide 504. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 322 to nucleotide 504, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from
15 nucleotide 322 to nucleotide 504, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 322 to nucleotide 504.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:76;
 - (b) fragments of the amino acid sequence of SEQ ID NO:76, each fragment comprising eight consecutive amino acids of SEQ ID NO:76; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone na474_10 deposited with the ATCC under accession number 98629;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:76. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino
30 acids of SEQ ID NO:76, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 66 to amino acid 75 of SEQ ID NO:76.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 92 to nucleotide 1435;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 170 to nucleotide 1435;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone nn16_10 deposited with the ATCC under accession number 98629;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone nn16_10 deposited with the ATCC under accession number 98629;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone nn16_10 deposited with the ATCC under accession number 98629;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone nn16_10 deposited with the ATCC under accession number 98629;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:78;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:77 from nucleotide 92 to nucleotide 1435; the nucleotide sequence of SEQ ID NO:77 from nucleotide 170 to nucleotide 1435; the nucleotide sequence of the full-length protein

coding sequence of clone nn16_10 deposited with the ATCC under accession number 98629; or the nucleotide sequence of a mature protein coding sequence of clone nn16_10 deposited with the ATCC under accession number 98629. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone nn16_10 deposited with the ATCC under accession number 98629. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:78, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 218 to amino acid 227 of SEQ ID NO:78.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:77.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and
 - (ab) the nucleotide sequence of the cDNA insert of clone nn16_10 deposited with the ATCC under accession number 98629;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

(bb) the nucleotide sequence of the cDNA insert of clone nn16_10 deposited with the ATCC under accession number 98629;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:77 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 92 to nucleotide 1435, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 92 to nucleotide 1435, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 92 to nucleotide 1435. Also preferably the polynucleotide isolated according to the above
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 170 to nucleotide 1435, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 170 to nucleotide 1435, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 170 to nucleotide 1435.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:78;

(b) fragments of the amino acid sequence of SEQ ID NO:78, each
30 fragment comprising eight consecutive amino acids of SEQ ID NO:78; and

(c) the amino acid sequence encoded by the cDNA insert of clone nn16_10 deposited with the ATCC under accession number 98629;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:78. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:78, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 218 to amino acid 227 of SEQ ID NO:78.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 1567 to nucleotide 1809;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 1726 to nucleotide 1809;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone np189_9 deposited with the ATCC under accession number 98629;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone np189_9 deposited with the ATCC under accession number 98629;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone np189_9 deposited with the ATCC under accession number 98629;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone np189_9 deposited with the ATCC under accession number 98629;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:80;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:80;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:79 from nucleotide 1567 to nucleotide 1809; the nucleotide sequence of SEQ ID NO:79 from nucleotide 1726 to nucleotide 1809; the nucleotide sequence of the full-length
10 protein coding sequence of clone np189_9 deposited with the ATCC under accession number 98629; or the nucleotide sequence of a mature protein coding sequence of clone np189_9 deposited with the ATCC under accession number 98629. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone np189_9 deposited with the ATCC under accession number
15 98629. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:80, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence
20 of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:80.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:79.

Further embodiments of the invention provide isolated polynucleotides produced
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

(ab) the nucleotide sequence of the cDNA insert of clone np189_9 deposited with the ATCC under accession number 98629;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

(bb) the nucleotide sequence of the cDNA insert of clone np189_9 deposited with the ATCC under accession number 98629;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79, and
20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 1567 to
25 nucleotide 1809, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 1567 to nucleotide 1809, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 1567 to nucleotide 1809. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the
30 cDNA sequence of SEQ ID NO:79 from nucleotide 1726 to nucleotide 1809, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 1726 to nucleotide 1809, to a nucleotide sequence

corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 1726 to nucleotide 1809.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:80;
- (b) fragments of the amino acid sequence of SEQ ID NO:80, each fragment comprising eight consecutive amino acids of SEQ ID NO:80; and
- (c) the amino acid sequence encoded by the cDNA insert of clone np189_9 deposited with the ATCC under accession number 98629;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:80. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:80, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:80.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 2054 to nucleotide 2206;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ny226_1 deposited with the ATCC under accession number 98629;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ny226_1 deposited with the ATCC under accession number 98629;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ny226_1 deposited with the ATCC under accession number 98629;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ny226_1 deposited with the ATCC under accession number 98629;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:82;

5 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:82;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

10 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
15 NO:81 from nucleotide 2054 to nucleotide 2206; the nucleotide sequence of the full-length protein coding sequence of clone ny226_1 deposited with the ATCC under accession number 98629; or the nucleotide sequence of a mature protein coding sequence of clone ny226_1 deposited with the ATCC under accession number 98629. In other preferred
20 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ny226_1 deposited with the ATCC under accession number 98629. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
25 SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:82, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 20 to amino acid 29 of SEQ ID NO:82.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:81.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(ab) the nucleotide sequence of the cDNA insert of clone ny226_1 deposited with the ATCC under accession number 98629;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

20 (bb) the nucleotide sequence of the cDNA insert of clone ny226_1 deposited with the ATCC under accession number 98629;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:81 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81. Also preferably the
30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 2054 to nucleotide 2206, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 2054 to nucleotide 2206,

to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 2054 to nucleotide 2206.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the
5 group consisting of:

- (a) the amino acid sequence of SEQ ID NO:82;
 - (b) fragments of the amino acid sequence of SEQ ID NO:82, each fragment comprising eight consecutive amino acids of SEQ ID NO:82; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 ny226_1 deposited with the ATCC under accession number 98629;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:82. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:82, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 20 to amino acid 29 of SEQ ID NO:82.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83 from nucleotide 567 to nucleotide 701;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pe159_1 deposited with the ATCC under
25 accession number 98629;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pe159_1 deposited with the ATCC under accession number
30 98629;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pe159_1 deposited with the ATCC under accession number 98629;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pe159_1 deposited with the ATCC under accession number 98629;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:84;

5 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:84;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

10 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:83 from nucleotide 567 to nucleotide 701; the nucleotide sequence of the full-length protein coding sequence of clone pe159_1 deposited with the ATCC under accession number 98629; or the nucleotide sequence of a mature protein coding sequence of clone pe159_1 deposited with the ATCC under accession number 98629. In other preferred
15 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pe159_1 deposited with the ATCC under accession number 98629. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:84, or
20 a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 17 to amino acid 26 of SEQ ID NO:84.
25

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:83.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83; and

(ab) the nucleotide sequence of the cDNA insert of clone pe159_1 deposited with the ATCC under accession number 98629;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83; and

20 (bb) the nucleotide sequence of the cDNA insert of clone pe159_1 deposited with the ATCC under accession number 98629;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:83 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83. Also preferably the
30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 567 to nucleotide 701, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from nucleotide 567 to nucleotide 701, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 567 to nucleotide 701.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the
5 group consisting of:

- (a) the amino acid sequence of SEQ ID NO:84;
- (b) fragments of the amino acid sequence of SEQ ID NO:84, each fragment comprising eight consecutive amino acids of SEQ ID NO:84; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
10 pe159_1 deposited with the ATCC under accession number 98629;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:84. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:84, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 17 to amino acid 26 of SEQ ID NO:84.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 593 to nucleotide 784;
- 25 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 698 to nucleotide 784;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pj314_8 deposited with the ATCC under accession number 98629;
- 30 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pj314_8 deposited with the ATCC under accession number 98629;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pj314_8 deposited with the ATCC under accession number 98629;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pj314_8 deposited with the ATCC under accession number 98629;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:86;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:86;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:85 from nucleotide 593 to nucleotide 784; the nucleotide sequence of SEQ ID NO:85 from nucleotide 698 to nucleotide 784; the nucleotide sequence of the full-length protein coding sequence of clone pj314_8 deposited with the ATCC under accession number 98629; or the nucleotide sequence of a mature protein coding sequence of clone pj314_8 deposited with the ATCC under accession number 98629. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pj314_8 deposited with the ATCC under accession number 98629. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:86, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 27 to amino acid 36 of SEQ ID NO:86.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:85.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

5 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

10 (ab) the nucleotide sequence of the cDNA insert of clone pj314_8 deposited with the ATCC under accession number 98629;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

15 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (ba) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

(bb) the nucleotide sequence of the cDNA insert of clone pj314_8 deposited with the ATCC under accession number 98629;

25 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:85 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide 593 to nucleotide 784, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 593 to nucleotide 784, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 593 to nucleotide 784. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide 698 to nucleotide 784, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 698 to nucleotide 784, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 698 to nucleotide 784.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:86;
- (b) fragments of the amino acid sequence of SEQ ID NO:86, each fragment comprising eight consecutive amino acids of SEQ ID NO:86; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pj314_8 deposited with the ATCC under accession number 98629;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:86. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:86, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 27 to amino acid 36 of SEQ ID NO:86.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 176 to nucleotide 328;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 239 to nucleotide 328;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 1 to nucleotide 512;

5 (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bp870_1 deposited with the ATCC under accession number 98724;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bp870_1 deposited with the ATCC under accession number
10 98724;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bp870_1 deposited with the ATCC under accession number 98724;

(h) a polynucleotide encoding a mature protein encoded by the cDNA
15 insert of clone bp870_1 deposited with the ATCC under accession number 98724;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:88;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment
20 comprising eight consecutive amino acids of SEQ ID NO:88;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and

25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:87 from nucleotide 176 to nucleotide 328; the nucleotide sequence of SEQ ID NO:87 from nucleotide 239 to nucleotide 328; the nucleotide sequence of SEQ ID NO:87 from
30 nucleotide 1 to nucleotide 512; the nucleotide sequence of the full-length protein coding sequence of clone bp870_1 deposited with the ATCC under accession number 98724; or the nucleotide sequence of a mature protein coding sequence of clone bp870_1 deposited with the ATCC under accession number 98724. In other preferred embodiments, the

polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bp870_1 deposited with the ATCC under accession number 98724. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:88, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 20 to amino acid 29 of SEQ ID NO:88.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:87.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and

(ab) the nucleotide sequence of the cDNA insert of clone bp870_1 deposited with the ATCC under accession number 98724;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and

(bb) the nucleotide sequence of the cDNA insert of clone
bp870_1 deposited with the ATCC under accession number 98724;
(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 65 degrees C;

- 5 (iii) amplifying human DNA sequences; and
(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
10 ID NO:87 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:87, but
excluding the poly(A) tail at the 3' end of SEQ ID NO:87. Also preferably the
polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 176 to nucleotide
328, and extending contiguously from a nucleotide sequence corresponding to the 5' end
15 of said sequence of SEQ ID NO:87 from nucleotide 176 to nucleotide 328, to a nucleotide
sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide
176 to nucleotide 328. Also preferably the polynucleotide isolated according to the above
process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
NO:87 from nucleotide 239 to nucleotide 328, and extending contiguously from a
20 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from
nucleotide 239 to nucleotide 328, to a nucleotide sequence corresponding to the 3' end of
said sequence of SEQ ID NO:87 from nucleotide 239 to nucleotide 328. Also preferably
the polynucleotide isolated according to the above process comprises a nucleotide
sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 1 to
25 nucleotide 512, and extending contiguously from a nucleotide sequence corresponding
to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 1 to nucleotide 512, to a
nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from
nucleotide 1 to nucleotide 512.

In other embodiments, the present invention provides a composition comprising
30 a protein, wherein said protein comprises an amino acid sequence selected from the
group consisting of:

- (a) the amino acid sequence of SEQ ID NO:88;

(b) fragments of the amino acid sequence of SEQ ID NO:88, each fragment comprising eight consecutive amino acids of SEQ ID NO:88; and

(c) the amino acid sequence encoded by the cDNA insert of clone bp870_1 deposited with the ATCC under accession number 98724;

- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino
10 acids of SEQ ID NO:88, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 20 to amino acid 29 of SEQ ID NO:88.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 15 to nucleotide 749;

- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 141 to nucleotide 749;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bx141_2 deposited with the ATCC under accession number 98630;

- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bx141_2 deposited with the ATCC under accession number 98630;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bx141_2 deposited with the ATCC under accession number 98630;

- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bx141_2 deposited with the ATCC under accession number 98630;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:90;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:90;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:89 from nucleotide 15 to nucleotide 749; the nucleotide sequence of SEQ ID NO:89 from nucleotide 141 to nucleotide 749; the nucleotide sequence of the full-length protein coding sequence of clone bx141_2 deposited with the ATCC under accession number 98630; or the nucleotide sequence of a mature protein coding sequence of clone bx141_2
15 deposited with the ATCC under accession number 98630. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bx141_2 deposited with the ATCC under accession number 98630. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:90
20 from amino acid 1 to amino acid 122. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:90, or a polynucleotide encoding a protein comprising a fragment of
25 the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:90.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:89.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

(ab) the nucleotide sequence of the cDNA insert of clone bx141_2 deposited with the ATCC under accession number 98630;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

20 (bb) the nucleotide sequence of the cDNA insert of clone bx141_2 deposited with the ATCC under accession number 98630;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:89 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89. Also preferably the
30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 15 to nucleotide 749, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 15 to nucleotide 749, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide 15 to nucleotide 749. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 141 to nucleotide 749, and extending contiguously from a
5 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 141 to nucleotide 749, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide 141 to nucleotide 749.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the
10 group consisting of:

- (a) the amino acid sequence of SEQ ID NO:90;
- (b) the amino acid sequence of SEQ ID NO:90 from amino acid 1 to amino acid 122;
- (c) fragments of the amino acid sequence of SEQ ID NO:90, each
15 fragment comprising eight consecutive amino acids of SEQ ID NO:90; and
- (d) the amino acid sequence encoded by the cDNA insert of clone bx141_2 deposited with the ATCC under accession number 98630;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:90 or the amino acid sequence
20 of SEQ ID NO:90 from amino acid 1 to amino acid 122. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:90, or a protein comprising a fragment of the amino acid sequence of SEQ ID
25 NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:90.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:91;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 100 to nucleotide 1767;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 280 to nucleotide 1767;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw272_7 deposited with the ATCC under accession number 98630;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw272_7 deposited with the ATCC under accession number 98630;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw272_7 deposited with the ATCC under accession number 98630;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw272_7 deposited with the ATCC under accession number 98630;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:92;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:92;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:91 from nucleotide 100 to nucleotide 1767; the nucleotide sequence of SEQ ID NO:91 from nucleotide 280 to nucleotide 1767; the nucleotide sequence of the full-length protein coding sequence of clone cw272_7 deposited with the ATCC under accession number 98630; or the nucleotide sequence of a mature protein coding sequence of clone cw272_7 deposited with the ATCC under accession number 98630. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw272_7 deposited with the ATCC under accession number 98630. In further preferred embodiments, the present invention provides a

polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:92, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 273 to amino acid 282 of SEQ ID NO:92.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:91.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and

(ab) the nucleotide sequence of the cDNA insert of clone cw272_7 deposited with the ATCC under accession number 98630;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and

(bb) the nucleotide sequence of the cDNA insert of clone cw272_7 deposited with the ATCC under accession number 98630;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:91 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91 from nucleotide
10 1767, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 100 to nucleotide 1767, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide 100 to nucleotide 1767. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of
15 SEQ ID NO:91 from nucleotide 280 to nucleotide 1767, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 280 to nucleotide 1767, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide 280 to nucleotide 1767.

In other embodiments, the present invention provides a composition comprising
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:92;
- (b) fragments of the amino acid sequence of SEQ ID NO:92, each fragment comprising eight consecutive amino acids of SEQ ID NO:92; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone cw272_7 deposited with the ATCC under accession number 98630;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:92. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:92, or a protein comprising a fragment of the amino acid sequence

of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 273 to amino acid 282 of SEQ ID NO:92.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 49 to nucleotide 1245;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:93 from nucleotide 265 to nucleotide 1245;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone nh328_5 deposited with the ATCC under accession number 98630;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone nh328_5 deposited with the ATCC under accession number 98630;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone nh328_5 deposited with the ATCC under accession number 98630;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone nh328_5 deposited with the ATCC under accession number 98630;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94;
- (i) a polynucleotide encoding a protein comprising a fragment of the
25 amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:94;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein
30 of (h) or (i) above ; and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:93 from nucleotide 49 to nucleotide 1245; the nucleotide sequence of SEQ ID NO:93 from nucleotide 265 to nucleotide 1245; the nucleotide sequence of the full-length protein coding sequence of clone nh328_5 deposited with the ATCC under accession number 98630; or the nucleotide sequence of a mature protein coding sequence of clone nh328_5 deposited with the ATCC under accession number 98630. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone nh328_5 deposited with the ATCC under accession number 98630. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94 from amino acid 229 to amino acid 387. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:94, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 194 to amino acid 203 of SEQ ID NO:94.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:93.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and
 - (ab) the nucleotide sequence of the cDNA insert of clone nh328_5 deposited with the ATCC under accession number 98630;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

10 (bb) the nucleotide sequence of the cDNA insert of clone nh328_5 deposited with the ATCC under accession number 98630;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:93 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:93, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:93. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 49 to nucleotide 1245, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 49 to nucleotide 1245, to a nucleotide
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 49 to nucleotide 1245. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 265 to nucleotide 1245, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from
30 nucleotide 265 to nucleotide 1245, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 265 to nucleotide 1245.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:94;
 - 5 (b) the amino acid sequence of SEQ ID NO:94 from amino acid 229 to amino acid 387;
 - (c) fragments of the amino acid sequence of SEQ ID NO:94, each fragment comprising eight consecutive amino acids of SEQ ID NO:94; and
 - (d) the amino acid sequence encoded by the cDNA insert of clone
 - 10 nh328_5 deposited with the ATCC under accession number 98630;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:94 or the amino acid sequence of SEQ ID NO:94 from amino acid 229 to amino acid 387. In further preferred
- embodiments, the present invention provides a protein comprising a fragment of the
- 15 amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:94, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 194 to amino acid 203 of SEQ ID NO:94.

20 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 25 NO:95 from nucleotide 166 to nucleotide 552;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone nm214_3 deposited with the ATCC under accession number 98630;
- (d) a polynucleotide encoding the full-length protein encoded by the
- 30 cDNA insert of clone nm214_3 deposited with the ATCC under accession number 98630;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone nm214_3 deposited with the ATCC under accession number 98630;

5 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone nm214_3 deposited with the ATCC under accession number 98630;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:96;

10 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:96;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and

15 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:95 from nucleotide 166 to nucleotide 552; the nucleotide sequence of the full-length protein coding sequence of clone nm214_3 deposited with the ATCC under accession
20 number 98630; or the nucleotide sequence of a mature protein coding sequence of clone nm214_3 deposited with the ATCC under accession number 98630. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone nm214_3 deposited with the ATCC under accession number 98630. In further preferred embodiments, the present invention provides a
25 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:96, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid
30 sequence from amino acid 59 to amino acid 68 of SEQ ID NO:96.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:95.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and

(ab) the nucleotide sequence of the cDNA insert of clone nm214_3 deposited with the ATCC under accession number 98630;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and

(bb) the nucleotide sequence of the cDNA insert of clone nm214_3 deposited with the ATCC under accession number 98630;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:95 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 166 to nucleotide 552, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 166 to nucleotide 552, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 166 to nucleotide 552.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:96;
- 10 (b) fragments of the amino acid sequence of SEQ ID NO:96, each fragment comprising eight consecutive amino acids of SEQ ID NO:96; and
- (c) the amino acid sequence encoded by the cDNA insert of clone nm214_3 deposited with the ATCC under accession number 98630;

the protein being substantially free from other mammalian proteins. Preferably such
15 protein comprises the amino acid sequence of SEQ ID NO:96. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:96, or a protein comprising a fragment of the amino acid sequence
20 of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 59 to amino acid 68 of SEQ ID NO:96.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:97;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 203 to nucleotide 1441;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 251 to nucleotide 1441;
- 30 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone nn320_2 deposited with the ATCC under accession number 98630;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone nn320_2 deposited with the ATCC under accession number 98630;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone nn320_2 deposited with the ATCC under accession number 98630;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone nn320_2 deposited with the ATCC under accession number 98630;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:98;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:98;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:97 from nucleotide 203 to nucleotide 1441; the nucleotide sequence of SEQ ID NO:97 from nucleotide 251 to nucleotide 1441; the nucleotide sequence of the full-length protein coding sequence of clone nn320_2 deposited with the ATCC under accession number 98630; or the nucleotide sequence of a mature protein coding sequence of clone nn320_2 deposited with the ATCC under accession number 98630. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone nn320_2 deposited with the ATCC under accession number 98630. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:98 from amino acid 1 to amino acid 92. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino

acids of SEQ ID NO:98, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 201 to amino acid 210 of SEQ ID NO:98.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:97.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and
 - 15 (ab) the nucleotide sequence of the cDNA insert of clone nn320_2 deposited with the ATCC under accession number 98630;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 20 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (ba) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and
 - (bb) the nucleotide sequence of the cDNA insert of clone nn320_2 deposited with the ATCC under accession number 98630;
 - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:97, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:97. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 203 to nucleotide 1441, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 203 to nucleotide 1441, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 203 to nucleotide 1441. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 251 to nucleotide 1441, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from
15 nucleotide 251 to nucleotide 1441, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 251 to nucleotide 1441.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:98;
- (b) the amino acid sequence of SEQ ID NO:98 from amino acid 1 to amino acid 92;
- (c) fragments of the amino acid sequence of SEQ ID NO:98, each fragment comprising eight consecutive amino acids of SEQ ID NO:98; and
- 25 (d) the amino acid sequence encoded by the cDNA insert of clone nn320_2 deposited with the ATCC under accession number 98630;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:98 or the amino acid sequence of SEQ ID NO:98 from amino acid 1 to amino acid 92. In further preferred embodiments,
30 the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:98, or a protein comprising a fragment of the amino acid sequence of SEQ ID

NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 201 to amino acid 210 of SEQ ID NO:98.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99 from nucleotide 74 to nucleotide 1531;
- (c) a polynucleotide comprising the nucleotide sequence of the full-
10 length protein coding sequence of clone pp392_3 deposited with the ATCC under accession number 98630;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pp392_3 deposited with the ATCC under accession number 98630;
- 15 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pp392_3 deposited with the ATCC under accession number 98630;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pp392_3 deposited with the ATCC under accession number 98630;
- 20 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:100;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:100;
- 25 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and
- (k) a polynucleotide that hybridizes under stringent conditions to any
30 one of the polynucleotides specified in (a)-(h).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:99 from nucleotide 74 to nucleotide 1531; the nucleotide sequence of the full-length protein coding sequence of clone pp392_3 deposited with the ATCC under accession

number 98630; or the nucleotide sequence of a mature protein coding sequence of clone pp392_3 deposited with the ATCC under accession number 98630. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pp392_3 deposited with the ATCC under accession number 98630. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:100, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 237 to amino acid 246 of SEQ ID NO:100.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:99.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

- (ab) the nucleotide sequence of the cDNA insert of clone pp392_3 deposited with the ATCC under accession number 98630;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

(bb) the nucleotide sequence of the cDNA insert of clone pp392_3 deposited with the ATCC under accession number 98630;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
ID NO:99 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:99, but
excluding the poly(A) tail at the 3' end of SEQ ID NO:99. Also preferably the
polynucleotide isolated according to the above process comprises a nucleotide sequence
15 corresponding to the cDNA sequence of SEQ ID NO:99 from nucleotide 74 to nucleotide
1531, and extending contiguously from a nucleotide sequence corresponding to the 5' end
of said sequence of SEQ ID NO:99 from nucleotide 74 to nucleotide 1531, to a nucleotide
sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide
74 to nucleotide 1531.

20 In other embodiments, the present invention provides a composition comprising
a protein, wherein said protein comprises an amino acid sequence selected from the
group consisting of:

(a) the amino acid sequence of SEQ ID NO:100;

(b) fragments of the amino acid sequence of SEQ ID NO:100, each
25 fragment comprising eight consecutive amino acids of SEQ ID NO:100; and

(c) the amino acid sequence encoded by the cDNA insert of clone
pp392_3 deposited with the ATCC under accession number 98630;

the protein being substantially free from other mammalian proteins. Preferably such
protein comprises the amino acid sequence of SEQ ID NO:100. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the
amino acid sequence of SEQ ID NO:100 having biological activity, the fragment
preferably comprising eight (more preferably twenty, most preferably thirty) consecutive
amino acids of SEQ ID NO:100, or a protein comprising a fragment of the amino acid

sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 237 to amino acid 246 of SEQ ID NO:100.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 58 to nucleotide 474;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 310 to nucleotide 474;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ya13_1 deposited with the ATCC under accession number 98630;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ya13_1 deposited with the ATCC under accession number 98630;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ya13_1 deposited with the ATCC under accession number 98630;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ya13_1 deposited with the ATCC under accession number 98630;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:102;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:101 from nucleotide 58 to nucleotide 474; the nucleotide sequence of SEQ ID NO:101 from nucleotide 310 to nucleotide 474; the nucleotide sequence of the full-length protein coding sequence of clone ya13_1 deposited with the ATCC under accession number 98630; or the nucleotide sequence of a mature protein coding sequence of clone ya13_1 deposited with the ATCC under accession number 98630. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ya13_1 deposited with the ATCC under accession number 98630.

In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:102, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 64 to amino acid 73 of SEQ ID NO:102.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:101.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (aa) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and
 - (ab) the nucleotide sequence of the cDNA insert of clone ya13_1 deposited with the ATCC under accession number 98630;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
 - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and
- (bb) the nucleotide sequence of the cDNA insert of clone ya13_1 deposited with the ATCC under accession number 98630;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;
- 10 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
15 ID NO:101 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 58 to nucleotide 474, and extending contiguously from a nucleotide sequence corresponding to the 5' end
20 of said sequence of SEQ ID NO:101 from nucleotide 58 to nucleotide 474, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 58 to nucleotide 474. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 310 to nucleotide 474, and extending contiguously from a
25 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from nucleotide 310 to nucleotide 474, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 310 to nucleotide 474.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the
30 group consisting of:

- (a) the amino acid sequence of SEQ ID NO:102;
- (b) fragments of the amino acid sequence of SEQ ID NO:102, each fragment comprising eight consecutive amino acids of SEQ ID NO:102; and

(c) the amino acid sequence encoded by the cDNA insert of clone ya13_1 deposited with the ATCC under accession number 98630; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:102. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:102, or a protein comprising a fragment of the amino acid
10 amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 64 to amino acid 73 of SEQ ID NO:102.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 76 to nucleotide 540;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 196 to nucleotide 540;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb37_1 deposited with the ATCC under
20 accession number 98630;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb37_1 deposited with the ATCC under accession number 98630;
- 25 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb37_1 deposited with the ATCC under accession number 98630;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb37_1 deposited with the ATCC under accession number 98630;
- 30 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:104;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:104;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:103 from nucleotide 76 to nucleotide 540; the nucleotide sequence of SEQ ID NO:103 from nucleotide 196 to nucleotide 540; the nucleotide sequence of the full-length protein coding sequence of clone yb37_1 deposited with the ATCC under accession number 98630; or the nucleotide sequence of a mature protein coding sequence of clone yb37_1
15 deposited with the ATCC under accession number 98630. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb37_1 deposited with the ATCC under accession number 98630. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
20 SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:104, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 72 to amino acid 81 of SEQ ID NO:104.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:103.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and

(ab) the nucleotide sequence of the cDNA insert of clone yb37_1 deposited with the ATCC under accession number 98630;

5 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

10 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (ba) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and

(bb) the nucleotide sequence of the cDNA insert of clone yb37_1 deposited with the ATCC under accession number 98630;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

20 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
25 ID NO:103 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 76 to nucleotide 540, and extending contiguously from a nucleotide sequence corresponding to the 5' end
30 of said sequence of SEQ ID NO:103 from nucleotide 76 to nucleotide 540, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 76 to nucleotide 540. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:103 from nucleotide 196 to nucleotide 540, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 196 to nucleotide 540, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 196 to nucleotide 540.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:104;
- (b) fragments of the amino acid sequence of SEQ ID NO:104, each
10 fragment comprising eight consecutive amino acids of SEQ ID NO:104; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yb37_1 deposited with the ATCC under accession number 98630;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:104. In further preferred
15 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:104, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the
20 amino acid sequence from amino acid 72 to amino acid 81 of SEQ ID NO:104.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 275 to nucleotide 415;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 374 to nucleotide 415;
- (d) a polynucleotide comprising the nucleotide sequence of the full-
30 length protein coding sequence of clone yb39_1 deposited with the ATCC under accession number 98630;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb39_1 deposited with the ATCC under accession number 98630;
- 5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb39_1 deposited with the ATCC under accession number 98630;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb39_1 deposited with the ATCC under accession number 98630;
- (h) a polynucleotide encoding a protein comprising the amino acid
10 sequence of SEQ ID NO:106;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:106;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of
15 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:105 from nucleotide 275 to nucleotide 415; the nucleotide sequence of SEQ ID NO:105 from nucleotide 374 to nucleotide 415; the nucleotide sequence of the full-length protein coding sequence of clone yb39_1 deposited with the ATCC under accession number 98630; or the nucleotide sequence of a mature protein coding sequence of clone yb39_1
25 deposited with the ATCC under accession number 98630. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb39_1 deposited with the ATCC under accession number 98630. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
30 SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:106, or a polynucleotide encoding a protein comprising a fragment of the amino acid

sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 15 to amino acid 24 of SEQ ID NO:106.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:105.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:105, but excluding the poly(A) tail at the
3' end of SEQ ID NO:105; and

(ab) the nucleotide sequence of the cDNA insert of clone
yb39_1 deposited with the ATCC under accession number 98630;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:105, but excluding the poly(A) tail at the
25 3' end of SEQ ID NO:105; and

(bb) the nucleotide sequence of the cDNA insert of clone yb39_1 deposited with the ATCC under accession number 98630;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105, and

extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:105 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
5 corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 275 to nucleotide 415, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 275 to nucleotide 415, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 275 to nucleotide 415. Also preferably the polynucleotide isolated
10 according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 374 to nucleotide 415, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 374 to nucleotide 415, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 374 to
15 nucleotide 415.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:106;
- 20 (b) fragments of the amino acid sequence of SEQ ID NO:106, each fragment comprising eight consecutive amino acids of SEQ ID NO:106; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yb39_1 deposited with the ATCC under accession number 98630;

the protein being substantially free from other mammalian proteins. Preferably such
25 protein comprises the amino acid sequence of SEQ ID NO:106. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:106, or a protein comprising a fragment of the amino acid
30 sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 15 to amino acid 24 of SEQ ID NO:106.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 427 to nucleotide 1146;

5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 589 to nucleotide 1146;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bd577_1 deposited with the ATCC under accession number 98631;

10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bd577_1 deposited with the ATCC under accession number 98631;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bd577_1 deposited with the ATCC under accession number 98631;

15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bd577_1 deposited with the ATCC under accession number 98631;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:108;

20 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:108;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

25 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:107 from nucleotide 427 to nucleotide 1146; the nucleotide sequence of SEQ ID NO:107 from nucleotide 589 to nucleotide 1146; the nucleotide sequence of the full-length protein coding sequence of clone bd577_1 deposited with the ATCC under accession number 98631; or the nucleotide sequence of a mature protein coding sequence of clone

bd577_1 deposited with the ATCC under accession number 98631. In other preferred
embodiments, the polynucleotide encodes the full-length or a mature protein encoded by
the cDNA insert of clone bd577_1 deposited with the ATCC under accession number
98631. In further preferred embodiments, the present invention provides a
5 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
SEQ ID NO:108 having biological activity, the fragment preferably comprising eight
(more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID
NO:108, or a polynucleotide encoding a protein comprising a fragment of the amino acid
sequence of SEQ ID NO:108 having biological activity, the fragment comprising the
10 amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:108.

Other embodiments provide the gene corresponding to the cDNA sequence of
SEQ ID NO:107.

Further embodiments of the invention provide isolated polynucleotides produced
according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize
in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
consisting of:
- (aa) SEQ ID NO:107, but excluding the poly(A) tail at the
20 3' end of SEQ ID NO:107; and
- (ab) the nucleotide sequence of the cDNA insert of clone
bd577_1 deposited with the ATCC under accession number 98631;
- (ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 65 degrees C; and
- 25 (iii) isolating the DNA polynucleotides detected with the
probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
30 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:
- (ba) SEQ ID NO:107, but excluding the poly(A) tail at the
3' end of SEQ ID NO:107; and

- (bb) the nucleotide sequence of the cDNA insert of clone
bd577_1 deposited with the ATCC under accession number 98631;
- (ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 65 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
10 ID NO:107 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:107, but
excluding the poly(A) tail at the 3' end of SEQ ID NO:107. Also preferably the
polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 427 to
nucleotide 1146, and extending contiguously from a nucleotide sequence corresponding
15 to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 427 to nucleotide 1146,
to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:107
from nucleotide 427 to nucleotide 1146. Also preferably the polynucleotide isolated
according to the above process comprises a nucleotide sequence corresponding to the
cDNA sequence of SEQ ID NO:107 from nucleotide 589 to nucleotide 1146, and extending
20 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of
SEQ ID NO:107 from nucleotide 589 to nucleotide 1146, to a nucleotide sequence
corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 589 to
nucleotide 1146.

In other embodiments, the present invention provides a composition comprising
25 a protein, wherein said protein comprises an amino acid sequence selected from the
group consisting of:

- (a) the amino acid sequence of SEQ ID NO:108;
- (b) fragments of the amino acid sequence of SEQ ID NO:108, each
fragment comprising eight consecutive amino acids of SEQ ID NO:108; and
- 30 (c) the amino acid sequence encoded by the cDNA insert of clone
bd577_1 deposited with the ATCC under accession number 98631;

the protein being substantially free from other mammalian proteins. Preferably such
protein comprises the amino acid sequence of SEQ ID NO:108. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:108, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:108.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 95 to nucleotide 1522;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 161 to nucleotide 1522;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bv280_3 deposited with the ATCC under accession number 98631;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bv280_3 deposited with the ATCC under accession number 98631;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bv280_3 deposited with the ATCC under accession number 98631;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bv280_3 deposited with the ATCC under accession number 98631;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:110;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:110;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

5 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:109 from nucleotide 95 to nucleotide 1522; the nucleotide sequence of SEQ ID NO:109 from nucleotide 161 to nucleotide 1522; the nucleotide sequence of the full-length protein coding sequence of clone bv280_3 deposited with the ATCC under accession number 98631; or the nucleotide sequence of a mature protein coding sequence of clone bv280_3
10 deposited with the ATCC under accession number 98631. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bv280_3 deposited with the ATCC under accession number 98631. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
15 SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:110, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 233 to amino acid 242 of SEQ ID NO:110.

20 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:109.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

25 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

30 (ab) the nucleotide sequence of the cDNA insert of clone bv280_3 deposited with the ATCC under accession number 98631;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

10 (bb) the nucleotide sequence of the cDNA insert of clone bv280_3 deposited with the ATCC under accession number 98631;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:109 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:109, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:109. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 95 to nucleotide 1522, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from nucleotide 95 to nucleotide 1522, to a nucleotide
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 95 to nucleotide 1522. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 161 to nucleotide 1522, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from
30 nucleotide 161 to nucleotide 1522, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 161 to nucleotide 1522.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:110;
- 5 (b) fragments of the amino acid sequence of SEQ ID NO:110, each fragment comprising eight consecutive amino acids of SEQ ID NO:110; and
- (c) the amino acid sequence encoded by the cDNA insert of clone bv280_3 deposited with the ATCC under accession number 98631;

the protein being substantially free from other mammalian proteins. Preferably such
10 protein comprises the amino acid sequence of SEQ ID NO:110. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:110, or a protein comprising a fragment of the amino acid
15 sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 233 to amino acid 242 of SEQ ID NO:110.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
20 NO:111;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 286 to nucleotide 552;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 475 to nucleotide 552;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone co315_3 deposited with the ATCC under accession number 98631;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone co315_3 deposited with the ATCC under accession number
30 98631;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone co315_3 deposited with the ATCC under accession number 98631;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone co315_3 deposited with the ATCC under accession number 98631;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112;

5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:112;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
15 NO:111 from nucleotide 286 to nucleotide 552; the nucleotide sequence of SEQ ID NO:111 from nucleotide 475 to nucleotide 552; the nucleotide sequence of the full-length protein coding sequence of clone co315_3 deposited with the ATCC under accession number 98631; or the nucleotide sequence of a mature protein coding sequence of clone co315_3 deposited with the ATCC under accession number 98631. In other preferred
20 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone co315_3 deposited with the ATCC under accession number 98631. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight
25 (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:112, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:112.

Other embodiments provide the gene corresponding to the cDNA sequence of
30 SEQ ID NO:111.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

(ab) the nucleotide sequence of the cDNA insert of clone co315_3 deposited with the ATCC under accession number 98631;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

20 (bb) the nucleotide sequence of the cDNA insert of clone co315_3 deposited with the ATCC under accession number 98631;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:111 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111. Also preferably the
30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 286 to nucleotide 552, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 286 to nucleotide 552,

to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 286 to nucleotide 552. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 475 to nucleotide 552, and extending
5 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 475 to nucleotide 552, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 475 to nucleotide 552.

In other embodiments, the present invention provides a composition comprising
10 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:112;
- (b) fragments of the amino acid sequence of SEQ ID NO:112, each fragment comprising eight consecutive amino acids of SEQ ID NO:112; and
15 (c) the amino acid sequence encoded by the cDNA insert of clone co315_3 deposited with the ATCC under accession number 98631;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:112. In further preferred
20 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:112, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:112.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:113 from nucleotide 1682 to nucleotide 1963;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ij226_6 deposited with the ATCC under accession number 98631;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ij226_6 deposited with the ATCC under accession number 98631;

5 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ij226_6 deposited with the ATCC under accession number 98631;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ij226_6 deposited with the ATCC under accession number 98631;

10 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:114;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:114;

15 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:113 from nucleotide 1682 to nucleotide 1963; the nucleotide sequence of the full-length protein coding sequence of clone ij226_6 deposited with the ATCC under accession number 98631; or the nucleotide sequence of a mature protein coding sequence of clone ij226_6 deposited with the ATCC under accession number 98631. In other preferred
25 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ij226_6 deposited with the ATCC under accession number 98631.

In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably
30 twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:114, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:114.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:113.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:113, but excluding the poly(A) tail at the
- 10 3' end of SEQ ID NO:113; and
- (ab) the nucleotide sequence of the cDNA insert of clone ij226_6 deposited with the ATCC under accession number 98631;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 ij226_6 deposited with the ATCC under accession number 98631;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:113 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:113, but

excluding the poly(A) tail at the 3' end of SEQ ID NO:113. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113 from nucleotide 1682 to nucleotide 1963, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 1682 to nucleotide 1963, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:113 from nucleotide 1682 to nucleotide 1963.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:114;
 - (b) fragments of the amino acid sequence of SEQ ID NO:114, each fragment comprising eight consecutive amino acids of SEQ ID NO:114; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone ij226_6 deposited with the ATCC under accession number 98631;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:114. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:114, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:114.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 1137 to nucleotide 1346;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone nf443_1 deposited with the ATCC under accession number 98631;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone nf443_1 deposited with the ATCC under accession number 98631;

5 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone nf443_1 deposited with the ATCC under accession number 98631;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone nf443_1 deposited with the ATCC under accession number 98631;

10 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:116;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:116;

15 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:115 from nucleotide 1137 to nucleotide 1346; the nucleotide sequence of the full-length protein coding sequence of clone nf443_1 deposited with the ATCC under accession number 98631; or the nucleotide sequence of a mature protein coding sequence of clone nf443_1 deposited with the ATCC under accession number 98631. In other
25 preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone nf443_1 deposited with the ATCC under accession number 98631. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight
30 (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:116, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 30 to amino acid 39 of SEQ ID NO:116.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:115.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:115, but excluding the poly(A) tail at the
- 10 3' end of SEQ ID NO:115; and
- (ab) the nucleotide sequence of the cDNA insert of clone nf443_1 deposited with the ATCC under accession number 98631;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 nf443_1 deposited with the ATCC under accession number 98631;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:115 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:115, but

excluding the poly(A) tail at the 3' end of SEQ ID NO:115. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115 from nucleotide 1137 to nucleotide 1346, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 1137 to nucleotide 1346, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:115 from nucleotide 1137 to nucleotide 1346.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:116;
- (b) fragments of the amino acid sequence of SEQ ID NO:116, each fragment comprising eight consecutive amino acids of SEQ ID NO:116; and
- (c) the amino acid sequence encoded by the cDNA insert of clone nf443_1 deposited with the ATCC under accession number 98631;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:116. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:116, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 30 to amino acid 39 of SEQ ID NO:116.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117 from nucleotide 308 to nucleotide 634;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone nt429_1 deposited with the ATCC under accession number 98631;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone nt429_1 deposited with the ATCC under accession number 98631;

5 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone nt429_1 deposited with the ATCC under accession number 98631;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone nt429_1 deposited with the ATCC under accession number 98631;

10 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:118;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:118;

15 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:117 from nucleotide 308 to nucleotide 634; the nucleotide sequence of the full-length protein coding sequence of clone nt429_1 deposited with the ATCC under accession number 98631; or the nucleotide sequence of a mature protein coding sequence of clone nt429_1 deposited with the ATCC under accession number 98631. In other preferred
25 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone nt429_1 deposited with the ATCC under accession number 98631. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:118 from amino acid 1 to amino acid 47. In further preferred embodiments, the present
30 invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:118, or a polynucleotide encoding a protein comprising a

fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino acid 49 to amino acid 58 of SEQ ID NO:118.

Other embodiments provide the gene corresponding to the cDNA sequence of
5 SEQ ID NO:117.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117; and

15 (ab) the nucleotide sequence of the cDNA insert of clone nt429_1 deposited with the ATCC under accession number 98631;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

20 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117; and

(bb) the nucleotide sequence of the cDNA insert of clone nt429_1 deposited with the ATCC under accession number 98631;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:117 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:117, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:117. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117 from nucleotide 308 to nucleotide 634, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:117 from nucleotide 308 to nucleotide 634,
10 to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:117 from nucleotide 308 to nucleotide 634.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:118;
- (b) the amino acid sequence of SEQ ID NO:118 from amino acid 1 to amino acid 47;
- (c) fragments of the amino acid sequence of SEQ ID NO:118, each fragment comprising eight consecutive amino acids of SEQ ID NO:118; and
- 20 (d) the amino acid sequence encoded by the cDNA insert of clone nt429_1 deposited with the ATCC under accession number 98631;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:118 or the amino acid sequence of SEQ ID NO:118 from amino acid 1 to amino acid 47. In further preferred embodiments,
25 the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:118, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid
30 sequence from amino acid 49 to amino acid 58 of SEQ ID NO:118.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:119;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:119 from nucleotide 104 to nucleotide 652;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:119 from nucleotide 377 to nucleotide 652;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pe503_1 deposited with the ATCC under accession number 98631;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pe503_1 deposited with the ATCC under accession number 98631;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pe503_1 deposited with the ATCC under accession number 98631;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pe503_1 deposited with the ATCC under accession number 98631;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:120;
- 20 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:120;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 25 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:119 from nucleotide 104 to nucleotide 652; the nucleotide sequence of SEQ ID NO:119 from nucleotide 377 to nucleotide 652; the nucleotide sequence of the full-length protein coding sequence of clone pe503_1 deposited with the ATCC under accession number 98631; or the nucleotide sequence of a mature protein coding sequence of clone pe503_1

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deposited with the ATCC under accession number 98631. In other preferred
embodiments, the polynucleotide encodes the full-length or a mature protein encoded by
the cDNA insert of clone pe503_1 deposited with the ATCC under accession number
98631. In yet other preferred embodiments, the present invention provides a
5 polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:120
from amino acid 69 to amino acid 125. In further preferred embodiments, the present
invention provides a polynucleotide encoding a protein comprising a fragment of the
amino acid sequence of SEQ ID NO:120 having biological activity, the fragment
preferably comprising eight (more preferably twenty, most preferably thirty) consecutive
10 amino acids of SEQ ID NO:120, or a polynucleotide encoding a protein comprising a
fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the
fragment comprising the amino acid sequence from amino acid 86 to amino acid 95 of
SEQ ID NO:120.

Other embodiments provide the gene corresponding to the cDNA sequence of
15 SEQ ID NO:119.

Further embodiments of the invention provide isolated polynucleotides produced
according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
20 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
consisting of:
 - (aa) SEQ ID NO:119, but excluding the poly(A) tail at the
3' end of SEQ ID NO:119; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
25 pe503_1 deposited with the ATCC under accession number 98631;
 - (ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 65 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the
probe(s);
- 30 and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119; and
- (bb) the nucleotide sequence of the cDNA insert of clone pe503_1 deposited with the ATCC under accession number 98631;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;
- 10 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:119, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

15 ID NO:119 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:119 from nucleotide 104 to nucleotide 652, and extending contiguously from a nucleotide sequence corresponding

20 to the 5' end of said sequence of SEQ ID NO:119 from nucleotide 104 to nucleotide 652, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:119 from nucleotide 104 to nucleotide 652. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:119 from nucleotide 377 to nucleotide 652, and extending

25 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:119 from nucleotide 377 to nucleotide 652, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:119 from nucleotide 377 to nucleotide 652.

In other embodiments, the present invention provides a composition comprising

30 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:120;

(b) the amino acid sequence of SEQ ID NO:120 from amino acid 69 to amino acid 125;

(c) fragments of the amino acid sequence of SEQ ID NO:120, each fragment comprising eight consecutive amino acids of SEQ ID NO:120; and

5 (d) the amino acid sequence encoded by the cDNA insert of clone pe503_1 deposited with the ATCC under accession number 98631;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:120 or the amino acid sequence of SEQ ID NO:120 from amino acid 69 to amino acid 125. In further preferred
10 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:120, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising the
15 amino acid sequence from amino acid 86 to amino acid 95 of SEQ ID NO:120.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121;

20 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121 from nucleotide 23 to nucleotide 442;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121 from nucleotide 224 to nucleotide 442;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pe834_6 deposited with the ATCC under
25 accession number 98631;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pe834_6 deposited with the ATCC under accession number 98631;

30 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pe834_6 deposited with the ATCC under accession number 98631;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pe834_6 deposited with the ATCC under accession number 98631;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:122;

5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:122;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
15 NO:121 from nucleotide 23 to nucleotide 442; the nucleotide sequence of SEQ ID NO:121 from nucleotide 224 to nucleotide 442; the nucleotide sequence of the full-length protein coding sequence of clone pe834_6 deposited with the ATCC under accession number 98631; or the nucleotide sequence of a mature protein coding sequence of clone pe834_6 deposited with the ATCC under accession number 98631. In other preferred
20 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pe834_6 deposited with the ATCC under accession number 98631. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment preferably comprising eight
25 (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:122, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:122.

Other embodiments provide the gene corresponding to the cDNA sequence of
30 SEQ ID NO:121.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121; and

(ab) the nucleotide sequence of the cDNA insert of clone pe834_6 deposited with the ATCC under accession number 98631;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121; and

20 (bb) the nucleotide sequence of the cDNA insert of clone pe834_6 deposited with the ATCC under accession number 98631;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:121, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:121 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121. Also preferably the
30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:121 from nucleotide 23 to nucleotide 442, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:121 from nucleotide 23 to nucleotide 442, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:121 from nucleotide 23 to nucleotide 442.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:122;
- (b) fragments of the amino acid sequence of SEQ ID NO:122, each fragment comprising eight consecutive amino acids of SEQ ID NO:122; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pe834_6 deposited with the ATCC under accession number 98631;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:122. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:122, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:122.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123 from nucleotide 98 to nucleotide 265;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123 from nucleotide 152 to nucleotide 265;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ya10_1 deposited with the ATCC under accession number 98631;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ya10_1 deposited with the ATCC under accession number 98631;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ya10_1 deposited with the ATCC under accession number 98631;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ya10_1 deposited with the ATCC under accession number 98631;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:124;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:124;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:123 from nucleotide 98 to nucleotide 265; the nucleotide sequence of SEQ ID NO:123 from nucleotide 152 to nucleotide 265; the nucleotide sequence of the full-length protein coding sequence of clone ya10_1 deposited with the ATCC under accession number 98631; or the nucleotide sequence of a mature protein coding sequence of clone ya10_1 deposited with the ATCC under accession number 98631. In other preferred
20 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ya10_1 deposited with the ATCC under accession number 98631.

25 In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:124, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
30 SEQ ID NO:124 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:124.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:123.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

5 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123; and

10 (ab) the nucleotide sequence of the cDNA insert of clone ya10_1 deposited with the ATCC under accession number 98631;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

15 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (ba) SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123; and

(bb) the nucleotide sequence of the cDNA insert of clone ya10_1 deposited with the ATCC under accession number 98631;

25 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:123, and
30 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:123 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the cDNA sequence of SEQ ID NO:123 from nucleotide 98 to nucleotide 265, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:123 from nucleotide 98 to nucleotide 265, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:123 from nucleotide 98 to nucleotide 265. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:123 from nucleotide 152 to nucleotide 265, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:123 from nucleotide 152 to nucleotide 265, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:123 from nucleotide 152 to nucleotide 265.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:124;
- (b) fragments of the amino acid sequence of SEQ ID NO:124, each fragment comprising eight consecutive amino acids of SEQ ID NO:124; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ya10_1 deposited with the ATCC under accession number 98631;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:124. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:124, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:124.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125 from nucleotide 176 to nucleotide 583;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb40_1 deposited with the ATCC under accession number 98631;

5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb40_1 deposited with the ATCC under accession number 98631;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb40_1 deposited with the ATCC under accession number 98631;

10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb40_1 deposited with the ATCC under accession number 98631;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:126;

15 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:126;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

20 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:125 from nucleotide 176 to nucleotide 583; the nucleotide sequence of the full-length
25 protein coding sequence of clone yb40_1 deposited with the ATCC under accession number 98631; or the nucleotide sequence of a mature protein coding sequence of clone yb40_1 deposited with the ATCC under accession number 98631. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb40_1 deposited with the ATCC under accession number
30 98631. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID

NO:126, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising the amino acid sequence from amino acid 63 to amino acid 72 of SEQ ID NO:126.

Other embodiments provide the gene corresponding to the cDNA sequence of
5 SEQ ID NO:125.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125; and

15 (ab) the nucleotide sequence of the cDNA insert of clone yb40_1 deposited with the ATCC under accession number 98631;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

20 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125; and

(bb) the nucleotide sequence of the cDNA insert of clone yb40_1 deposited with the ATCC under accession number 98631;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:125 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:125, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:125. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125 from nucleotide 176 to nucleotide 583, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:125 from nucleotide 176 to nucleotide 583,
10 to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:125 from nucleotide 176 to nucleotide 583.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:126;
 - (b) fragments of the amino acid sequence of SEQ ID NO:126, each fragment comprising eight consecutive amino acids of SEQ ID NO:126; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone yb40_1 deposited with the ATCC under accession number 98631;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:126. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive
25 amino acids of SEQ ID NO:126, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising the amino acid sequence from amino acid 63 to amino acid 72 of SEQ ID NO:126.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127 from nucleotide 734 to nucleotide 1873;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127 from nucleotide 1403 to nucleotide 1873;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cs756_2 deposited with the ATCC under accession number 98636;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cs756_2 deposited with the ATCC under accession number 98636;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cs756_2 deposited with the ATCC under accession number 98636;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cs756_2 deposited with the ATCC under accession number 98636;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:128;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:128;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:127 from nucleotide 734 to nucleotide 1873; the nucleotide sequence of SEQ ID NO:127 from nucleotide 1403 to nucleotide 1873; the nucleotide sequence of the full-length protein coding sequence of clone cs756_2 deposited with the ATCC under accession number 98636; or the nucleotide sequence of a mature protein coding sequence of clone cs756_2 deposited with the ATCC under accession number 98636. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cs756_2 deposited with the ATCC under accession number 98636. In further preferred embodiments, the present invention provides a

polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:128, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising the amino acid sequence from amino acid 185 to amino acid 194 of SEQ ID NO:128.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:127.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127; and

(ab) the nucleotide sequence of the cDNA insert of clone cs756_2 deposited with the ATCC under accession number 98636;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127; and

(bb) the nucleotide sequence of the cDNA insert of clone cs756_2 deposited with the ATCC under accession number 98636;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:127 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127 from nucleotide 734 to
10 nucleotide 1873, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:127 from nucleotide 734 to nucleotide 1873, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:127 from nucleotide 734 to nucleotide 1873. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the
15 cDNA sequence of SEQ ID NO:127 from nucleotide 1403 to nucleotide 1873, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:127 from nucleotide 1403 to nucleotide 1873, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:127 from nucleotide 1403 to nucleotide 1873.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:128;
- (b) fragments of the amino acid sequence of SEQ ID NO:128, each
25 fragment comprising eight consecutive amino acids of SEQ ID NO:128; and
- (c) the amino acid sequence encoded by the cDNA insert of clone cs756_2 deposited with the ATCC under accession number 98636;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:128. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:128, or a protein comprising a fragment of the amino acid

sequence of SEQ ID NO:128 having biological activity, the fragment comprising the amino acid sequence from amino acid 185 to amino acid 194 of SEQ ID NO:128.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129 from nucleotide 26 to nucleotide 1738;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:129 from nucleotide 140 to nucleotide 1738;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ew150_1 deposited with the ATCC under accession number 98636;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone ew150_1 deposited with the ATCC under accession number 98636;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ew150_1 deposited with the ATCC under accession number 98636;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ew150_1 deposited with the ATCC under accession number 98636;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:130;
- (i) a polynucleotide encoding a protein comprising a fragment of the
25 amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:130;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein
30 of (h) or (i) above ; and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:129 from nucleotide 26 to nucleotide 1738; the nucleotide sequence of SEQ ID NO:129 from nucleotide 140 to nucleotide 1738; the nucleotide sequence of the full-length protein coding sequence of clone ew150_1 deposited with the ATCC under accession number 98636; or the nucleotide sequence of a mature protein coding sequence of clone ew150_1 deposited with the ATCC under accession number 98636. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ew150_1 deposited with the ATCC under accession number 98636. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:130 from amino acid 108 to amino acid 166. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:130, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising the amino acid sequence from amino acid 280 to amino acid 289 of SEQ ID NO:130.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:129.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:129, but excluding the poly(A) tail at the 3' end of SEQ ID NO:129; and
 - (ab) the nucleotide sequence of the cDNA insert of clone ew150_1 deposited with the ATCC under accession number 98636;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:129, but excluding the poly(A) tail at the 3' end of SEQ ID NO:129; and

(bb) the nucleotide sequence of the cDNA insert of clone ew150_1 deposited with the ATCC under accession number 98636;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:129 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:129, but excluding the poly(A) tail at the 3' end of SEQ ID NO:129. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129 from nucleotide 26 to nucleotide 1738, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:129 from nucleotide 26 to nucleotide 1738, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:129 from nucleotide 26 to nucleotide 1738. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129 from nucleotide 140 to nucleotide 1738, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:129 from nucleotide 140 to nucleotide 1738, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:129 from nucleotide 140 to nucleotide 1738.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:130;
 - 5 (b) the amino acid sequence of SEQ ID NO:130 from amino acid 108 to amino acid 166;
 - (c) fragments of the amino acid sequence of SEQ ID NO:130, each fragment comprising eight consecutive amino acids of SEQ ID NO:130; and
 - (d) the amino acid sequence encoded by the cDNA insert of clone
10 ew150_1 deposited with the ATCC under accession number 98636;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:130 or the amino acid sequence of SEQ ID NO:130 from amino acid 108 to amino acid 166. In further preferred
15 amino acid sequence of SEQ ID NO:130 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:130, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising the amino acid sequence from amino acid 280 to amino acid 289 of SEQ ID NO:130.

20 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:131 from nucleotide 1101 to nucleotide 1910;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131 from nucleotide 1260 to nucleotide 1910;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone gg894_13 deposited with the ATCC under
30 accession number 98636;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone gg894_13 deposited with the ATCC under accession number 98636;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone gg894_13 deposited with the ATCC under accession number 98636;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone gg894_13 deposited with the ATCC under accession number 98636;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:132;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:132;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:131 from nucleotide 1101 to nucleotide 1910; the nucleotide sequence of SEQ ID NO:131 from nucleotide 1260 to nucleotide 1910; the nucleotide sequence of the full-length protein coding sequence of clone gg894_13 deposited with the ATCC under accession number 98636; or the nucleotide sequence of a mature protein coding sequence of clone gg894_13 deposited with the ATCC under accession number 98636. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone gg894_13 deposited with the ATCC under accession
20 number 98636. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:132, or a polynucleotide encoding a protein comprising a fragment of the amino acid
25 sequence of SEQ ID NO:132 having biological activity, the fragment comprising the amino acid sequence from amino acid 130 to amino acid 139 of SEQ ID NO:132.

30 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:131.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

5 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131; and

10 (ab) the nucleotide sequence of the cDNA insert of clone gg894_13 deposited with the ATCC under accession number 98636;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131; and

25 (bb) the nucleotide sequence of the cDNA insert of clone gg894_13 deposited with the ATCC under accession number 98636;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:131, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:131 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:131, but

excluding the poly(A) tail at the 3' end of SEQ ID NO:131. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:131 from nucleotide 1101 to nucleotide 1910, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 1101 to nucleotide 1910, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 1101 to nucleotide 1910. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:131 from nucleotide 1260 to nucleotide 1910, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 1260 to nucleotide 1910, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 1260 to nucleotide 1910.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:132;
- (b) fragments of the amino acid sequence of SEQ ID NO:132, each fragment comprising eight consecutive amino acids of SEQ ID NO:132; and
- (c) the amino acid sequence encoded by the cDNA insert of clone gg894_13 deposited with the ATCC under accession number 98636;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:132. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:132, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising the amino acid sequence from amino acid 130 to amino acid 139 of SEQ ID NO:132.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:133;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:133 from nucleotide 452 to nucleotide 1102;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone it217_2 deposited with the ATCC under accession number 98636;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone it217_2 deposited with the ATCC under accession number 98636;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone it217_2 deposited with the ATCC under accession number 98636;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone it217_2 deposited with the ATCC under accession number 98636;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:134;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:134;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:133 from nucleotide 452 to nucleotide 1102; the nucleotide sequence of the full-length protein coding sequence of clone it217_2 deposited with the ATCC under accession number 98636; or the nucleotide sequence of a mature protein coding sequence of clone it217_2 deposited with the ATCC under accession number 98636. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone it217_2 deposited with the ATCC under accession number 98636. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:134 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:134, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising the
5 amino acid sequence from amino acid 103 to amino acid 112 of SEQ ID NO:134.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:133.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 1.0 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:133, but excluding the poly(A) tail at the
1.5 3' end of SEQ ID NO:133; and
- (ab) the nucleotide sequence of the cDNA insert of clone it217_2 deposited with the ATCC under accession number 98636;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
- 2.0 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
2.5 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:133, but excluding the poly(A) tail at the 3' end of SEQ ID NO:133; and
- (bb) the nucleotide sequence of the cDNA insert of clone
3.0 it217_2 deposited with the ATCC under accession number 98636;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;
- (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:133 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:133, but excluding the poly(A) tail at the 3' end of SEQ ID NO:133. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133 from nucleotide 452 to nucleotide 1102, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:133 from nucleotide 452 to nucleotide 1102, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:133 from nucleotide 452 to nucleotide 1102.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:134;
- (b) fragments of the amino acid sequence of SEQ ID NO:134, each fragment comprising eight consecutive amino acids of SEQ ID NO:134; and
- (c) the amino acid sequence encoded by the cDNA insert of clone it217_2 deposited with the ATCC under accession number 98636;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:134. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:134, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising the amino acid sequence from amino acid 103 to amino acid 112 of SEQ ID NO:134.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:135;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:135 from nucleotide 127 to nucleotide 387;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:135 from nucleotide 172 to nucleotide 387;

5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ml235_2 deposited with the ATCC under accession number 98636;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ml235_2 deposited with the ATCC under accession number
10 98636;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ml235_2 deposited with the ATCC under accession number 98636;

(g) a polynucleotide encoding a mature protein encoded by the cDNA
15 insert of clone ml235_2 deposited with the ATCC under accession number 98636;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:136;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment
20 comprising eight consecutive amino acids of SEQ ID NO:136;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:135 from nucleotide 127 to nucleotide 387; the nucleotide sequence of SEQ ID NO:135 from nucleotide 172 to nucleotide 387; the nucleotide sequence of the full-length protein
30 coding sequence of clone ml235_2 deposited with the ATCC under accession number 98636; or the nucleotide sequence of a mature protein coding sequence of clone ml235_2 deposited with the ATCC under accession number 98636. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by

the cDNA insert of clone ml235_2 deposited with the ATCC under accession number 98636. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment preferably comprising eight
5 (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:136, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:136.

Other embodiments provide the gene corresponding to the cDNA sequence of
10 SEQ ID NO:135.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
15 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:135, but excluding the poly(A) tail at the
3' end of SEQ ID NO:135; and

(ab) the nucleotide sequence of the cDNA insert of clone
20 ml235_2 deposited with the ATCC under accession number 98636;

(ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the
probe(s);

25 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:

(ba) SEQ ID NO:135, but excluding the poly(A) tail at the
30 3' end of SEQ ID NO:135; and

(bb) the nucleotide sequence of the cDNA insert of clone
ml235_2 deposited with the ATCC under accession number 98636;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:135, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:135 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:135, but excluding the poly(A) tail at the 3' end of SEQ ID NO:135. Also preferably the
10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:135 from nucleotide 127 to nucleotide 387, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:135 from nucleotide 127 to nucleotide 387, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:135
15 from nucleotide 127 to nucleotide 387. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:135 from nucleotide 172 to nucleotide 387, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:135 from nucleotide 172 to nucleotide 387, to a nucleotide sequence
20 corresponding to the 3' end of said sequence of SEQ ID NO:135 from nucleotide 172 to nucleotide 387.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 25 (a) the amino acid sequence of SEQ ID NO:136;
(b) fragments of the amino acid sequence of SEQ ID NO:136, each fragment comprising eight consecutive amino acids of SEQ ID NO:136; and
(c) the amino acid sequence encoded by the cDNA insert of clone ml235_2 deposited with the ATCC under accession number 98636;

30 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:136. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment

preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:136, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:136.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:137;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:137 from nucleotide 147 to nucleotide 1163;
- 10 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:137 from nucleotide 273 to nucleotide 1163;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone mt24_2 deposited with the ATCC under accession number 98636;
- 15 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone mt24_2 deposited with the ATCC under accession number 98636;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone mt24_2 deposited with the ATCC under accession number 98636;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone mt24_2 deposited with the ATCC under accession number 98636;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:138;
- 25 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:138;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 30 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:137 from nucleotide 147 to nucleotide 1163; the nucleotide sequence of SEQ ID NO:137 from nucleotide 273 to nucleotide 1163; the nucleotide sequence of the full-length protein coding sequence of clone mt24_2 deposited with the ATCC under accession number 98636; or the nucleotide sequence of a mature protein coding sequence of clone mt24_2 deposited with the ATCC under accession number 98636. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone mt24_2 deposited with the ATCC under accession number 98636. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:138, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment comprising the amino acid sequence from amino acid 164 to amino acid 173 of SEQ ID NO:138.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:137.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:137, but excluding the poly(A) tail at the 3' end of SEQ ID NO:137; and

(ab) the nucleotide sequence of the cDNA insert of clone mt24_2 deposited with the ATCC under accession number 98636;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:137, but excluding the poly(A) tail at the 3' end of SEQ ID NO:137; and

(bb) the nucleotide sequence of the cDNA insert of clone mt24_2 deposited with the ATCC under accession number 98636;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:137, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:137 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:137, but excluding the poly(A) tail at the 3' end of SEQ ID NO:137. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the cDNA sequence of SEQ ID NO:137 from nucleotide 147 to nucleotide 1163, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:137 from nucleotide 147 to nucleotide 1163, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:137 from nucleotide 147 to nucleotide 1163. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:137 from nucleotide 273 to nucleotide 1163, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:137 from nucleotide 273 to nucleotide 1163, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:137 from nucleotide 273 to nucleotide 1163.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:138;
(b) fragments of the amino acid sequence of SEQ ID NO:138, each fragment comprising eight consecutive amino acids of SEQ ID NO:138; and
(c) the amino acid sequence encoded by the cDNA insert of clone
5 mt24_2 deposited with the ATCC under accession number 98636;
the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:138. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment
10 preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:138, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment comprising the amino acid sequence from amino acid 164 to amino acid 173 of SEQ ID NO:138.

In one embodiment, the present invention provides a composition comprising an
15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:139;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:139 from nucleotide 320 to nucleotide 1681;
- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:139 from nucleotide 437 to nucleotide 1681;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pe584_2 deposited with the ATCC under accession number 98636;
- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pe584_2 deposited with the ATCC under accession number 98636;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pe584_2 deposited with the ATCC under
30 accession number 98636;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pe584_2 deposited with the ATCC under accession number 98636;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:140;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:140;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:139 from nucleotide 320 to nucleotide 1681; the nucleotide sequence of SEQ ID NO:139 from nucleotide 437 to nucleotide 1681; the nucleotide sequence of the full-length protein coding sequence of clone pe584_2 deposited with the ATCC under accession number 98636; or the nucleotide sequence of a mature protein coding sequence of clone pe584_2 deposited with the ATCC under accession number 98636. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pe584_2 deposited with the ATCC under accession number 98636. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:140, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the fragment comprising the amino acid sequence from amino acid 222 to amino acid 231 of SEQ ID NO:140.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:139.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (aa) SEQ ID NO:139, but excluding the poly(A) tail at the 3' end of SEQ ID NO:139; and
- (ab) the nucleotide sequence of the cDNA insert of clone pe584_2 deposited with the ATCC under accession number 98636;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
- 10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 15 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:139, but excluding the poly(A) tail at the 3' end of SEQ ID NO:139; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 20 pe584_2 deposited with the ATCC under accession number 98636;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:139, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:139 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:139, but excluding the poly(A) tail at the 3' end of SEQ ID NO:139. Also preferably the

30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:139 from nucleotide 320 to nucleotide 1681, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:139 from nucleotide 320 to nucleotide 1681,

to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:139 from nucleotide 320 to nucleotide 1681. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:139 from nucleotide 437 to nucleotide 1681, and extending
5 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:139 from nucleotide 437 to nucleotide 1681, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:139 from nucleotide 437 to nucleotide 1681.

In other embodiments, the present invention provides a composition comprising
10 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:140;
- (b) fragments of the amino acid sequence of SEQ ID NO:140, each fragment comprising eight consecutive amino acids of SEQ ID NO:140; and
15 (c) the amino acid sequence encoded by the cDNA insert of clone pe584_2 deposited with the ATCC under accession number 98636;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:140. In further preferred
20 amino acid sequence of SEQ ID NO:140 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:140, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the fragment comprising the amino acid sequence from amino acid 222 to amino acid 231 of SEQ ID NO:140.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:141;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:141 from nucleotide 78 to nucleotide 1502;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:141 from nucleotide 564 to nucleotide 1502;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pj323_2 deposited with the ATCC under accession number 98636;

5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pj323_2 deposited with the ATCC under accession number 98636;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pj323_2 deposited with the ATCC under accession number 98636;

10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pj323_2 deposited with the ATCC under accession number 98636;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:142;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:142;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:141 from nucleotide 78 to nucleotide 1502; the nucleotide sequence of SEQ ID NO:141
25 from nucleotide 564 to nucleotide 1502; the nucleotide sequence of the full-length protein coding sequence of clone pj323_2 deposited with the ATCC under accession number 98636; or the nucleotide sequence of a mature protein coding sequence of clone pj323_2 deposited with the ATCC under accession number 98636. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by
30 the cDNA insert of clone pj323_2 deposited with the ATCC under accession number 98636. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:142 from amino acid 54 to amino acid 145. In further preferred embodiments, the present

invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:142, or a polynucleotide encoding a protein comprising a
5 fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment comprising the amino acid sequence from amino acid 232 to amino acid 241 of SEQ ID NO:142.

Other embodiments provide the gene corresponding to the cDNA sequence of
SEQ ID NO:141.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
15 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:141, but excluding the poly(A) tail at the
3' end of SEQ ID NO:141; and

(ab) the nucleotide sequence of the cDNA insert of clone
pj323_2 deposited with the ATCC under accession number 98636;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the
probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:

(ba) SEQ ID NO:141, but excluding the poly(A) tail at the
30 3' end of SEQ ID NO:141; and

(bb) the nucleotide sequence of the cDNA insert of clone
pj323_2 deposited with the ATCC under accession number 98636;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:141, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:141 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:141, but excluding the poly(A) tail at the 3' end of SEQ ID NO:141. Also preferably the
10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:141 from nucleotide 78 to nucleotide 1502, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:141 from nucleotide 78 to nucleotide 1502, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:141 from nucleotide
15 78 to nucleotide 1502. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:141 from nucleotide 564 to nucleotide 1502, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:141 from nucleotide 564 to nucleotide 1502, to a nucleotide sequence corresponding to the 3' end
20 of said sequence of SEQ ID NO:141 from nucleotide 564 to nucleotide 1502.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:142;
- 25 (b) the amino acid sequence of SEQ ID NO:142 from amino acid 54 to amino acid 145;
- (c) fragments of the amino acid sequence of SEQ ID NO:142, each fragment comprising eight consecutive amino acids of SEQ ID NO:142; and
- (d) the amino acid sequence encoded by the cDNA insert of clone
30 pj323_2 deposited with the ATCC under accession number 98636;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:142 or the amino acid sequence of SEQ ID NO:142 from amino acid 54 to amino acid 145. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:142, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment comprising the amino acid sequence from amino acid 232 to amino acid 241 of SEQ ID NO:142.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:143;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:143 from nucleotide 130 to nucleotide 294;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:143 from nucleotide 241 to nucleotide 294;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb24_1 deposited with the ATCC under accession number 98636;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb24_1 deposited with the ATCC under accession number 98636;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb24_1 deposited with the ATCC under accession number 98636;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb24_1 deposited with the ATCC under accession number 98636;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:144;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:144;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

5 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:143 from nucleotide 130 to nucleotide 294; the nucleotide sequence of SEQ ID NO:143 from nucleotide 241 to nucleotide 294; the nucleotide sequence of the full-length protein coding sequence of clone yb24_1 deposited with the ATCC under accession number 98636; or the nucleotide sequence of a mature protein coding sequence of clone yb24_1
10 deposited with the ATCC under accession number 98636. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb24_1 deposited with the ATCC under accession number 98636. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
15 SEQ ID NO:144 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:144, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:144.

20 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:143.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:
25 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:143, but excluding the poly(A) tail at the 3' end of SEQ ID NO:143; and

30 (ab) the nucleotide sequence of the cDNA insert of clone yb24_1 deposited with the ATCC under accession number 98636;
(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:143, but excluding the poly(A) tail at the 3' end of SEQ ID NO:143; and

10 (bb) the nucleotide sequence of the cDNA insert of clone yb24_1 deposited with the ATCC under accession number 98636;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:143, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:143 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:143, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:143. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:143 from nucleotide 130 to nucleotide 294, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:143 from nucleotide 130 to nucleotide 294,
25 to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:143 from nucleotide 130 to nucleotide 294. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:143 from nucleotide 241 to nucleotide 294, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of
30 SEQ ID NO:143 from nucleotide 241 to nucleotide 294, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:143 from nucleotide 241 to nucleotide 294.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:144;
- 5 (b) fragments of the amino acid sequence of SEQ ID NO:144, each fragment comprising eight consecutive amino acids of SEQ ID NO:144; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yb24_1 deposited with the ATCC under accession number 98636;

the protein being substantially free from other mammalian proteins. Preferably such
10 protein comprises the amino acid sequence of SEQ ID NO:144. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:144, or a protein comprising a fragment of the amino acid
15 sequence of SEQ ID NO:144 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:144.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
20 NO:145;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:145 from nucleotide 514 to nucleotide 1707;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:145 from nucleotide 580 to nucleotide 1707;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yb44_1 deposited with the ATCC under accession number 98636;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yb44_1 deposited with the ATCC under accession number
30 98636;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yb44_1 deposited with the ATCC under accession number 98636;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yb44_1 deposited with the ATCC under accession number 98636;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:146;

5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:146;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
15 NO:145 from nucleotide 514 to nucleotide 1707; the nucleotide sequence of SEQ ID NO:145 from nucleotide 580 to nucleotide 1707; the nucleotide sequence of the full-length protein coding sequence of clone yb44_1 deposited with the ATCC under accession number 98636; or the nucleotide sequence of a mature protein coding sequence of clone yb44_1 deposited with the ATCC under accession number 98636. In other preferred
20 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yb44_1 deposited with the ATCC under accession number 98636. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment preferably comprising eight
25 (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:146, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment comprising the amino acid sequence from amino acid 194 to amino acid 203 of SEQ ID NO:146.

Other embodiments provide the gene corresponding to the cDNA sequence of
30 SEQ ID NO:145.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:145, but excluding the poly(A) tail at the 3' end of SEQ ID NO:145; and

(ab) the nucleotide sequence of the cDNA insert of clone yb44_1 deposited with the ATCC under accession number 98636;

10 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:145, but excluding the poly(A) tail at the 3' end of SEQ ID NO:145; and

20 (bb) the nucleotide sequence of the cDNA insert of clone yb44_1 deposited with the ATCC under accession number 98636;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:145, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:145 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:145, but excluding the poly(A) tail at the 3' end of SEQ ID NO:145. Also preferably the
30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:145 from nucleotide 514 to nucleotide 1707, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:145 from nucleotide 514 to nucleotide 1707,

to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:145 from nucleotide 514 to nucleotide 1707. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:145 from nucleotide 580 to nucleotide 1707, and extending
5 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:145 from nucleotide 580 to nucleotide 1707, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:145 from nucleotide 580 to nucleotide 1707.

In other embodiments, the present invention provides a composition comprising
10 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:146;
- (b) fragments of the amino acid sequence of SEQ ID NO:146, each fragment comprising eight consecutive amino acids of SEQ ID NO:146; and
15 (c) the amino acid sequence encoded by the cDNA insert of clone yb44_1 deposited with the ATCC under accession number 98636;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:146. In further preferred
20 amino acid sequence of SEQ ID NO:146 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:146, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment comprising the amino acid sequence from amino acid 194 to amino acid 203 of SEQ ID NO:146.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:147;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:147 from nucleotide 1529 to nucleotide 1726;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:147 from nucleotide 1706 to nucleotide 1726;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bn69_15 deposited with the ATCC under accession number 98647;

5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bn69_15 deposited with the ATCC under accession number 98647;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bn69_15 deposited with the ATCC under accession number 98647;

10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bn69_15 deposited with the ATCC under accession number 98647;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:148;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:148;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:147 from nucleotide 1529 to nucleotide 1726; the nucleotide sequence of SEQ ID NO:147 from nucleotide 1706 to nucleotide 1726; the nucleotide sequence of the full-length protein coding sequence of clone bn69_15 deposited with the ATCC under accession number 98647; or the nucleotide sequence of a mature protein coding sequence of clone bn69_15 deposited with the ATCC under accession number 98647. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bn69_15 deposited with the ATCC under accession number 98647. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:148 from amino acid 1 to amino acid 53. In further preferred embodiments, the present

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invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:148, or a polynucleotide encoding a protein comprising a
5 fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment comprising the amino acid sequence from amino acid 28 to amino acid 37 of SEQ ID NO:148.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:147.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
15 consisting of:

(aa) SEQ ID NO:147, but excluding the poly(A) tail at the 3' end of SEQ ID NO:147; and

(ab) the nucleotide sequence of the cDNA insert of clone bn69_15 deposited with the ATCC under accession number 98647;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:147, but excluding the poly(A) tail at the 3' end of SEQ ID NO:147; and

(bb) the nucleotide sequence of the cDNA insert of clone bn69_15 deposited with the ATCC under accession number 98647;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:147, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:147 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:147, but excluding the poly(A) tail at the 3' end of SEQ ID NO:147. Also preferably the
- 10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:147 from nucleotide 1529 to nucleotide 1726, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:147 from nucleotide 1529 to nucleotide 1726, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:147
- 15 from nucleotide 1529 to nucleotide 1726. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:147 from nucleotide 1706 to nucleotide 1726, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:147 from nucleotide 1706 to nucleotide 1726, to a nucleotide
- 20 sequence corresponding to the 3' end of said sequence of SEQ ID NO:147 from nucleotide 1706 to nucleotide 1726.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 25 (a) the amino acid sequence of SEQ ID NO:148;
- (b) the amino acid sequence of SEQ ID NO:148 from amino acid 1 to amino acid 53;
- (c) fragments of the amino acid sequence of SEQ ID NO:148, each fragment comprising eight consecutive amino acids of SEQ ID NO:148; and
- 30 (d) the amino acid sequence encoded by the cDNA insert of clone bn69_15 deposited with the ATCC under accession number 98647;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:148 or the amino acid sequence

of SEQ ID NO:148 from amino acid 1 to amino acid 53. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:148, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment comprising the amino acid sequence from amino acid 28 to amino acid 37 of SEQ ID NO:148.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:149;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:149 from nucleotide 334 to nucleotide 597;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:149 from nucleotide 478 to nucleotide 597;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cb110_1 deposited with the ATCC under accession number 98647;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cb110_1 deposited with the ATCC under accession number 98647;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cb110_1 deposited with the ATCC under accession number 98647;
- 25 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cb110_1 deposited with the ATCC under accession number 98647;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:150;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:150;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

5 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:149 from nucleotide 334 to nucleotide 597; the nucleotide sequence of SEQ ID NO:149 from nucleotide 478 to nucleotide 597; the nucleotide sequence of the full-length protein coding sequence of clone cb110_1 deposited with the ATCC under accession number 98647; or the nucleotide sequence of a mature protein coding sequence of clone cb110_1
10 deposited with the ATCC under accession number 98647. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cb110_1 deposited with the ATCC under accession number 98647. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
15 SEQ ID NO:150 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:150, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:150.

20 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:149.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

25 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:149, but excluding the poly(A) tail at the 3' end of SEQ ID NO:149; and

30 (ab) the nucleotide sequence of the cDNA insert of clone cb110_1 deposited with the ATCC under accession number 98647;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:149, but excluding the poly(A) tail at the 3' end of SEQ ID NO:149; and

(bb) the nucleotide sequence of the cDNA insert of clone cb110_1 deposited with the ATCC under accession number 98647;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:149, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:149 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:149, but excluding the poly(A) tail at the 3' end of SEQ ID NO:149. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:149 from nucleotide 334 to nucleotide 597, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:149 from nucleotide 334 to nucleotide 597, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:149 from nucleotide 334 to nucleotide 597. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:149 from nucleotide 478 to nucleotide 597, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:149 from nucleotide 478 to nucleotide 597, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:149 from nucleotide 478 to nucleotide 597.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:150;
- 5 (b) fragments of the amino acid sequence of SEQ ID NO:150, each fragment comprising eight consecutive amino acids of SEQ ID NO:150; and
- (c) the amino acid sequence encoded by the cDNA insert of clone cb110_1 deposited with the ATCC under accession number 98647;

the protein being substantially free from other mammalian proteins. Preferably such
10 protein comprises the amino acid sequence of SEQ ID NO:150. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive
15 amino acids of SEQ ID NO:150, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:150.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
20 NO:151;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:151 from nucleotide 191 to nucleotide 1132;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:151 from nucleotide 290 to nucleotide 1132;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ch4_11 deposited with the ATCC under accession number 98647;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ch4_11 deposited with the ATCC under accession number
30 98647;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ch4_11 deposited with the ATCC under accession number 98647;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ch4_11 deposited with the ATCC under accession number 98647;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:152;

5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:152;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
15 NO:151 from nucleotide 191 to nucleotide 1132; the nucleotide sequence of SEQ ID NO:151 from nucleotide 290 to nucleotide 1132; the nucleotide sequence of the full-length protein coding sequence of clone ch4_11 deposited with the ATCC under accession number 98647; or the nucleotide sequence of a mature protein coding sequence of clone ch4_11 deposited with the ATCC under accession number 98647. In other preferred
20 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ch4_11 deposited with the ATCC under accession number 98647.

In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment preferably comprising eight (more preferably
25 twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:152, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment comprising the amino acid sequence from amino acid 152 to amino acid 161 of SEQ ID NO:152.

Other embodiments provide the gene corresponding to the cDNA sequence of
30 SEQ ID NO:151.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:151, but excluding the poly(A) tail at the 3' end of SEQ ID NO:151; and

(ab) the nucleotide sequence of the cDNA insert of clone ch4_11 deposited with the ATCC under accession number 98647;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:151, but excluding the poly(A) tail at the 3' end of SEQ ID NO:151; and

20 (bb) the nucleotide sequence of the cDNA insert of clone ch4_11 deposited with the ATCC under accession number 98647;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:151, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:151 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:151, but excluding the poly(A) tail at the 3' end of SEQ ID NO:151. Also preferably the
30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:151 from nucleotide 191 to nucleotide 1132, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:151 from nucleotide 191 to nucleotide 1132,

to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:151 from nucleotide 191 to nucleotide 1132. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:151 from nucleotide 290 to nucleotide 1132, and extending
5 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:151 from nucleotide 290 to nucleotide 1132, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:151 from nucleotide 290 to nucleotide 1132.

In other embodiments, the present invention provides a composition comprising
10 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:152;
- (b) fragments of the amino acid sequence of SEQ ID NO:152, each fragment comprising eight consecutive amino acids of SEQ ID NO:152; and
15 (c) the amino acid sequence encoded by the cDNA insert of clone ch4_11 deposited with the ATCC under accession number 98647;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:152. In further preferred
20 amino acid sequence of SEQ ID NO:152 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:152, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment comprising the amino acid sequence from amino acid 152 to amino acid 161 of SEQ ID NO:152.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:153;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:153 from nucleotide 732 to nucleotide 1898;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cn621_8 deposited with the ATCC under accession number 98647;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cn621_8 deposited with the ATCC under accession number 98647;

5 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cn621_8 deposited with the ATCC under accession number 98647;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cn621_8 deposited with the ATCC under accession number 98647;

10 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:154;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:154;

15 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:153 from nucleotide 732 to nucleotide 1898; the nucleotide sequence of the full-length protein coding sequence of clone cn621_8 deposited with the ATCC under accession number 98647; or the nucleotide sequence of a mature protein coding sequence of clone cn621_8 deposited with the ATCC under accession number 98647. In other preferred
25 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cn621_8 deposited with the ATCC under accession number 98647. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment preferably comprising eight
30 (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:154, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment comprising the amino acid sequence from amino acid 189 to amino acid 198 of SEQ ID NO:154.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:153.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:153, but excluding the poly(A) tail at the
 - 10 3' end of SEQ ID NO:153; and
 - (ab) the nucleotide sequence of the cDNA insert of clone cn621_8 deposited with the ATCC under accession number 98647;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
 - 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that
 - 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:153, but excluding the poly(A) tail at the 3' end of SEQ ID NO:153; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
 - 25 cn621_8 deposited with the ATCC under accession number 98647;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:153, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:153 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:153, but

excluding the poly(A) tail at the 3' end of SEQ ID NO:153. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:153 from nucleotide 732 to nucleotide 1898, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:153 from nucleotide 732 to nucleotide 1898, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:153 from nucleotide 732 to nucleotide 1898.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:154;
 - (b) fragments of the amino acid sequence of SEQ ID NO:154, each fragment comprising eight consecutive amino acids of SEQ ID NO:154; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone cn621_8 deposited with the ATCC under accession number 98647;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:154. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:154, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment comprising the amino acid sequence from amino acid 189 to amino acid 198 of SEQ ID NO:154.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:155;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:155 from nucleotide 308 to nucleotide 592;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:155 from nucleotide 377 to nucleotide 592;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone gy621_1 deposited with the ATCC under accession number 98647;

5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone gy621_1 deposited with the ATCC under accession number 98647;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone gy621_1 deposited with the ATCC under accession number 98647;

10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone gy621_1 deposited with the ATCC under accession number 98647;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:156;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:156;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:155 from nucleotide 308 to nucleotide 592; the nucleotide sequence of SEQ ID NO:155
25 from nucleotide 377 to nucleotide 592; the nucleotide sequence of the full-length protein coding sequence of clone gy621_1 deposited with the ATCC under accession number 98647; or the nucleotide sequence of a mature protein coding sequence of clone gy621_1 deposited with the ATCC under accession number 98647. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by
30 the cDNA insert of clone gy621_1 deposited with the ATCC under accession number 98647. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment preferably comprising eight

(more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:156, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:156.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:155.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:155, but excluding the poly(A) tail at the 3' end of SEQ ID NO:155; and
 - 15 (ab) the nucleotide sequence of the cDNA insert of clone gy621_1 deposited with the ATCC under accession number 98647;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the
 - 20 probe(s);
 - and
 - (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
 - 25 the group consisting of:
 - (ba) SEQ ID NO:155, but excluding the poly(A) tail at the 3' end of SEQ ID NO:155; and
 - (bb) the nucleotide sequence of the cDNA insert of clone gy621_1 deposited with the ATCC under accession number 98647;
 - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:155 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:155, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:155. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155 from nucleotide 308 to nucleotide 592, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:155 from nucleotide 308 to nucleotide 592,
10 to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:155 from nucleotide 308 to nucleotide 592. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155 from nucleotide 377 to nucleotide 592, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of
15 SEQ ID NO:155 from nucleotide 377 to nucleotide 592, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:155 from nucleotide 377 to nucleotide 592.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the
20 group consisting of:

- (a) the amino acid sequence of SEQ ID NO:156;
- (b) fragments of the amino acid sequence of SEQ ID NO:156, each fragment comprising eight consecutive amino acids of SEQ ID NO:156; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
25 gy621_1 deposited with the ATCC under accession number 98647;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:156. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment
30 preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:156, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:156.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:157;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:157 from nucleotide 124 to nucleotide 1881;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:157 from nucleotide 325 to nucleotide 1881;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone hb1041_2 deposited with the ATCC under
10 accession number 98647;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone hb1041_2 deposited with the ATCC under accession number 98647;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone hb1041_2 deposited with the ATCC under accession number 98647;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone hb1041_2 deposited with the ATCC under accession number 98647;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:158;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:158;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide that hybridizes under stringent conditions to any
30 one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:157 from nucleotide 124 to nucleotide 1881; the nucleotide sequence of SEQ ID NO:157 from nucleotide 325 to nucleotide 1881; the nucleotide sequence of the full-length

protein coding sequence of clone hb1041_2 deposited with the ATCC under accession number 98647; or the nucleotide sequence of a mature protein coding sequence of clone hb1041_2 deposited with the ATCC under accession number 98647. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone hb1041_2 deposited with the ATCC under accession number 98647. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:158, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment comprising the amino acid sequence from amino acid 288 to amino acid 297 of SEQ ID NO:158.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:157.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157; and

(ab) the nucleotide sequence of the cDNA insert of clone hb1041_2 deposited with the ATCC under accession number 98647;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157; and

(bb) the nucleotide sequence of the cDNA insert of clone hb1041_2 deposited with the ATCC under accession number 98647;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:157, and
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:157 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:157 from nucleotide 124 to
20 nucleotide 1881, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:157 from nucleotide 124 to nucleotide 1881, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:157 from nucleotide 124 to nucleotide 1881. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the
25 cDNA sequence of SEQ ID NO:157 from nucleotide 325 to nucleotide 1881, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:157 from nucleotide 325 to nucleotide 1881, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:157 from nucleotide 325 to nucleotide 1881.

30 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:158;

(b) fragments of the amino acid sequence of SEQ ID NO:158, each fragment comprising eight consecutive amino acids of SEQ ID NO:158; and

(c) the amino acid sequence encoded by the cDNA insert of clone hb1041_2 deposited with the ATCC under accession number 98647;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:158. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive
10 amino acids of SEQ ID NO:158, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment comprising the amino acid sequence from amino acid 288 to amino acid 297 of SEQ ID NO:158.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:159;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:159 from nucleotide 163 to nucleotide 1431;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone mh703_1 deposited with the ATCC under
20 accession number 98647;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone mh703_1 deposited with the ATCC under accession number 98647;

25 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone mh703_1 deposited with the ATCC under accession number 98647;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone mh703_1 deposited with the ATCC under accession number 98647;

30 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:160;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:160;

5 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ; and

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h).

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:159 from nucleotide 163 to nucleotide 1431; the nucleotide sequence of the full-length protein coding sequence of clone mh703_1 deposited with the ATCC under accession number 98647; or the nucleotide sequence of a mature protein coding sequence of clone mh703_1 deposited with the ATCC under accession number 98647. In other preferred
15 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone mh703_1 deposited with the ATCC under accession number 98647. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment preferably comprising eight
20 (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:160, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment comprising the amino acid sequence from amino acid 206 to amino acid 215 of SEQ ID NO:160.

Other embodiments provide the gene corresponding to the cDNA sequence of
25 SEQ ID NO:159.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize
30 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:159, but excluding the poly(A) tail at the 3' end of SEQ ID NO:159; and

- (ab) the nucleotide sequence of the cDNA insert of clone mh703_1 deposited with the ATCC under accession number 98647;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:159, but excluding the poly(A) tail at the 3' end of SEQ ID NO:159; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 mh703_1 deposited with the ATCC under accession number 98647;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:159, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:159 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:159, but excluding the poly(A) tail at the 3' end of SEQ ID NO:159. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:159 from nucleotide 163 to nucleotide 1431, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:159 from nucleotide 163 to nucleotide 1431, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:159
- 30 from nucleotide 163 to nucleotide 1431.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:160;
 - (b) fragments of the amino acid sequence of SEQ ID NO:160, each fragment comprising eight consecutive amino acids of SEQ ID NO:160; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone mh703_1 deposited with the ATCC under accession number 98647;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:160. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment
- 10 preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:160, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment comprising the amino acid sequence from amino acid 206 to amino acid 215 of SEQ ID NO:160.

In one embodiment, the present invention provides a composition comprising an

15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:161;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:161 from nucleotide 653 to nucleotide 934;
- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:161 from nucleotide 878 to nucleotide 934;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone na461_19 deposited with the ATCC under accession number 98647;
- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone na461_19 deposited with the ATCC under accession number 98647;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone na461_19 deposited with the ATCC under
- 30 accession number 98647;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone na461_19 deposited with the ATCC under accession number 98647;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:162;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:162 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:162;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:161 from nucleotide 653 to nucleotide 934; the nucleotide sequence of SEQ ID NO:161 from nucleotide 878 to nucleotide 934; the nucleotide sequence of the full-length protein coding sequence of clone na461_19 deposited with the ATCC under accession number 98647; or the nucleotide sequence of a mature protein coding sequence of clone na461_19 deposited with the ATCC under accession number 98647. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone na461_19 deposited with the ATCC under accession number 98647. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:162 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:162, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:162 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:162.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:161.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:161, but excluding the poly(A) tail at the 3' end of SEQ ID NO:161; and

(ab) the nucleotide sequence of the cDNA insert of clone na461_19 deposited with the ATCC under accession number 98647;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:161, but excluding the poly(A) tail at the 3' end of SEQ ID NO:161; and

(bb) the nucleotide sequence of the cDNA insert of clone na461_19 deposited with the ATCC under accession number 98647;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:161, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:161 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:161, but excluding the poly(A) tail at the 3' end of SEQ ID NO:161. Also preferably the
30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:161 from nucleotide 653 to nucleotide 934, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:161 from nucleotide 653 to nucleotide 934,

to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:161 from nucleotide 653 to nucleotide 934. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:161 from nucleotide 878 to nucleotide 934, and extending
5 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:161 from nucleotide 878 to nucleotide 934, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:161 from nucleotide 878 to nucleotide 934.

In other embodiments, the present invention provides a composition comprising
10 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:162;
- (b) fragments of the amino acid sequence of SEQ ID NO:162, each fragment comprising eight consecutive amino acids of SEQ ID NO:162; and
15 (c) the amino acid sequence encoded by the cDNA insert of clone na461_19 deposited with the ATCC under accession number 98647;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:162. In further preferred
20 amino acid sequence of SEQ ID NO:162 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:162, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:162 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:162.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:163;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:163 from nucleotide 72 to nucleotide 1319;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:163 from nucleotide 1071 to nucleotide 1319;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone na492_2 deposited with the ATCC under accession number 98647;

5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone na492_2 deposited with the ATCC under accession number 98647;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone na492_2 deposited with the ATCC under accession number 98647;

10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone na492_2 deposited with the ATCC under accession number 98647;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:164;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:164 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:164;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:163 from nucleotide 72 to nucleotide 1319; the nucleotide sequence of SEQ ID NO:163
25 from nucleotide 1071 to nucleotide 1319; the nucleotide sequence of the full-length protein coding sequence of clone na492_2 deposited with the ATCC under accession number 98647; or the nucleotide sequence of a mature protein coding sequence of clone na492_2 deposited with the ATCC under accession number 98647. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by
30 the cDNA insert of clone na492_2 deposited with the ATCC under accession number 98647. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:164 having biological activity, the fragment preferably comprising eight

(more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:164, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:164 having biological activity, the fragment comprising the amino acid sequence from amino acid 202 to amino acid 211 of SEQ ID NO:164.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:163.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:163, but excluding the poly(A) tail at the 3' end of SEQ ID NO:163; and
 - 15 (ab) the nucleotide sequence of the cDNA insert of clone na492_2 deposited with the ATCC under accession number 98647;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
 - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - 25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:163, but excluding the poly(A) tail at the 3' end of SEQ ID NO:163; and
 - (bb) the nucleotide sequence of the cDNA insert of clone na492_2 deposited with the ATCC under accession number 98647;
 - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:163, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:163 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:163, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:163. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:163 from nucleotide 72 to nucleotide 1319, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:163 from nucleotide 72 to nucleotide 1319, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:163 from nucleotide 72 to nucleotide 1319. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:163 from nucleotide 1071 to nucleotide 1319, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:163 from
15 nucleotide 1071 to nucleotide 1319, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:163 from nucleotide 1071 to nucleotide 1319.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:164;
 - (b) fragments of the amino acid sequence of SEQ ID NO:164, each fragment comprising eight consecutive amino acids of SEQ ID NO:164; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone na492_2 deposited with the ATCC under accession number 98647;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:164. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:164 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive
30 amino acids of SEQ ID NO:164, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:164 having biological activity, the fragment comprising the amino acid sequence from amino acid 202 to amino acid 211 of SEQ ID NO:164.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:165;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:165 from nucleotide 2848 to nucleotide 3048;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:165 from nucleotide 3004 to nucleotide 3048;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone na669_10 deposited with the ATCC under accession number 98647;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone na669_10 deposited with the ATCC under accession number 98647;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone na669_10 deposited with the ATCC under accession number 98647;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone na669_10 deposited with the ATCC under accession number 98647;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:166;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:166 having biological activity, the fragment comprising eight consecutive amino acids of SEQ ID NO:166;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:165 from nucleotide 2848 to nucleotide 3048; the nucleotide sequence of SEQ ID NO:165 from nucleotide 3004 to nucleotide 3048; the nucleotide sequence of the full-

length protein coding sequence of clone na669_10 deposited with the ATCC under accession number 98647; or the nucleotide sequence of a mature protein coding sequence of clone na669_10 deposited with the ATCC under accession number 98647. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone na669_10 deposited with the ATCC under accession number 98647. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:166 from amino acid 5 to amino acid 62. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:166 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:166, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:166 having biological activity, the fragment comprising the amino acid sequence from amino acid 28 to amino acid 37 of SEQ ID NO:166.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:165.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (aa) SEQ ID NO:165, but excluding the poly(A) tail at the 3' end of SEQ ID NO:165; and
 - (ab) the nucleotide sequence of the cDNA insert of clone na669_10 deposited with the ATCC under accession number 98647;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C; and
 - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:165, but excluding the poly(A) tail at the 3' end of SEQ ID NO:165; and

(bb) the nucleotide sequence of the cDNA insert of clone na669_10 deposited with the ATCC under accession number 98647;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 65 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:165, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
15 ID NO:165 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:165, but excluding the poly(A) tail at the 3' end of SEQ ID NO:165. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:165 from nucleotide 2848 to nucleotide 3048, and extending contiguously from a nucleotide sequence corresponding
20 to the 5' end of said sequence of SEQ ID NO:165 from nucleotide 2848 to nucleotide 3048, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:165 from nucleotide 2848 to nucleotide 3048. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:165 from nucleotide 3004 to nucleotide 3048, and
25 extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:165 from nucleotide 3004 to nucleotide 3048, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:165 from nucleotide 3004 to nucleotide 3048.

In other embodiments, the present invention provides a composition comprising
30 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:166;

(b) the amino acid sequence of SEQ ID NO:166 from amino acid 5 to amino acid 62;

(c) fragments of the amino acid sequence of SEQ ID NO:166, each fragment comprising eight consecutive amino acids of SEQ ID NO:166; and

5 (d) the amino acid sequence encoded by the cDNA insert of clone na669_10 deposited with the ATCC under accession number 98647;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:166 or the amino acid sequence of SEQ ID NO:166 from amino acid 5 to amino acid 62. In further preferred embodiments,
10 the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:166 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) consecutive amino acids of SEQ ID NO:166, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:166 having biological activity, the fragment comprising the amino acid
15 sequence from amino acid 28 to amino acid 37 of SEQ ID NO:166.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167;

20 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167 from nucleotide 185 to nucleotide 1678;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167 from nucleotide 482 to nucleotide 1678;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone co821_31 deposited with the ATCC under
25 accession number 98663;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone co821_31 deposited with the ATCC under accession number 98663;

30 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone co821_31 deposited with the ATCC under accession number 98663;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone co821_31 deposited with the ATCC under accession number 98663;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:168;

5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:168;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any
15 one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:167.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:167 from nucleotide 185 to nucleotide 1678; the nucleotide sequence of SEQ ID NO:167 from nucleotide 482 to nucleotide 1678; the nucleotide sequence of the full-length
20 protein coding sequence of clone co821_31 deposited with the ATCC under accession number 98663; or the nucleotide sequence of a mature protein coding sequence of clone co821_31 deposited with the ATCC under accession number 98663. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone co821_31 deposited with the ATCC under accession number
25 98663. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:168, or a polynucleotide encoding a protein comprising a fragment of the amino acid
30 sequence of SEQ ID NO:168 having biological activity, the fragment comprising the amino acid sequence from amino acid 244 to amino acid 253 of SEQ ID NO:168.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:167.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:167, but excluding the poly(A) tail at the 3' end of SEQ ID NO:167; and

(ab) the nucleotide sequence of the cDNA insert of clone co821_31 deposited with the ATCC under accession number 98663;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:167, but excluding the poly(A) tail at the 3' end of SEQ ID NO:167; and

(bb) the nucleotide sequence of the cDNA insert of clone co821_31 deposited with the ATCC under accession number 98663;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:167 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:167, but excluding the poly(A) tail at the 3' end of SEQ ID NO:167. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the cDNA sequence of SEQ ID NO:167 from nucleotide 185 to nucleotide 1678, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:167 from nucleotide 185 to nucleotide 1678, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:167 from nucleotide 185 to nucleotide 1678. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167 from nucleotide 482 to nucleotide 1678, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:167 from nucleotide 482 to nucleotide 1678, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:167 from nucleotide 482 to nucleotide 1678.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:168;
- (b) a fragment of the amino acid sequence of SEQ ID NO:168, the fragment comprising eight contiguous amino acids of SEQ ID NO:168; and
- (c) the amino acid sequence encoded by the cDNA insert of clone co821_31 deposited with the ATCC under accession number 98663;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:168. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous
- 25 amino acids of SEQ ID NO:168, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment comprising the amino acid sequence from amino acid 244 to amino acid 253 of SEQ ID NO:168.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:169;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:169 from nucleotide 176 to nucleotide 754;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:169 from nucleotide 425 to nucleotide 754;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dk329_1 deposited with the ATCC under accession number 98663;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dk329_1 deposited with the ATCC under accession number 98663;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dk329_1 deposited with the ATCC under accession number 98663;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dk329_1 deposited with the ATCC under accession number 98663;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:170;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:170;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:169.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:169 from nucleotide 176 to nucleotide 754; the nucleotide sequence of SEQ ID NO:169 from nucleotide 425 to nucleotide 754; the nucleotide sequence of the full-length protein coding sequence of clone dk329_1 deposited with the ATCC under accession number 98663; or the nucleotide sequence of a mature protein coding sequence of clone dk329_1 deposited with the ATCC under accession number 98663. In other preferred

embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dk329_1 deposited with the ATCC under accession number 98663. In further preferred embodiments, the present invention provides a

5 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:170, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment comprising the amino acid sequence from amino acid 91 to amino acid 100 of SEQ ID NO:170.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:169.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:
15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:169, but excluding the poly(A) tail at the 3' end of SEQ ID NO:169; and

20 (ab) the nucleotide sequence of the cDNA insert of clone dk329_1 deposited with the ATCC under accession number 98663;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

25 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:
(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
30 the group consisting of:

(ba) SEQ ID NO:169, but excluding the poly(A) tail at the 3' end of SEQ ID NO:169; and

- (bb) the nucleotide sequence of the cDNA insert of clone dk329_1 deposited with the ATCC under accession number 98663;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:169, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:169 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:169, but excluding the poly(A) tail at the 3' end of SEQ ID NO:169. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:169 from nucleotide 176 to nucleotide 754, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:169 from nucleotide 176 to nucleotide 754, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:169 from nucleotide 176 to nucleotide 754. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:169 from nucleotide 425 to nucleotide 754, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:169 from nucleotide 425 to nucleotide 754, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:169 from nucleotide 425 to nucleotide 754.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:170;
- (b) a fragment of the amino acid sequence of SEQ ID NO:170, the fragment comprising eight contiguous amino acids of SEQ ID NO:170; and
- 30 (c) the amino acid sequence encoded by the cDNA insert of clone dk329_1 deposited with the ATCC under accession number 98663;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:170. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:170, or a protein comprising a fragment of the amino acid
5 sequence of SEQ ID NO:170 having biological activity, the fragment comprising the amino acid sequence from amino acid 91 to amino acid 100 of SEQ ID NO:170.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171 from nucleotide 190 to nucleotide 1449;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171 from nucleotide 913 to nucleotide 1449;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fx317_11 deposited with the ATCC under accession number 98663;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fx317_11 deposited with the ATCC under accession number
20 98663;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fx317_11 deposited with the ATCC under accession number 98663;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
25 insert of clone fx317_11 deposited with the ATCC under accession number 98663;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:172;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment
30 comprising eight contiguous amino acids of SEQ ID NO:172;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

5 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:171.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:171 from nucleotide 190 to nucleotide 1449; the nucleotide sequence of SEQ ID
10 NO:171 from nucleotide 913 to nucleotide 1449; the nucleotide sequence of the full-length protein coding sequence of clone fx317_11 deposited with the ATCC under accession number 98663; or the nucleotide sequence of a mature protein coding sequence of clone fx317_11 deposited with the ATCC under accession number 98663. In other preferred
15 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fx317_11 deposited with the ATCC under accession number 98663. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
20 SEQ ID NO:172 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:172, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment comprising the amino acid sequence from amino acid 205 to amino acid 214 of SEQ ID NO:172.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:171.

25 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
30 consisting of:

(aa) SEQ ID NO:171, but excluding the poly(A) tail at the 3' end of SEQ ID NO:171; and

- (ab) the nucleotide sequence of the cDNA insert of clone
fx317_11 deposited with the ATCC under accession number 98663;
- (ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the
probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:
- (ba) SEQ ID NO:171, but excluding the poly(A) tail at the
3' end of SEQ ID NO:171; and
- (bb) the nucleotide sequence of the cDNA insert of clone
15 fx317_11 deposited with the ATCC under accession number 98663;
- (ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:171, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
ID NO:171 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:171, but
excluding the poly(A) tail at the 3' end of SEQ ID NO:171. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:171 from nucleotide 190 to
nucleotide 1449, and extending contiguously from a nucleotide sequence corresponding
to the 5' end of said sequence of SEQ ID NO:171 from nucleotide 190 to nucleotide 1449,
to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:171
- 30 from nucleotide 190 to nucleotide 1449. Also preferably the polynucleotide isolated
according to the above process comprises a nucleotide sequence corresponding to the
cDNA sequence of SEQ ID NO:171 from nucleotide 913 to nucleotide 1449, and extending
contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of

SEQ ID NO:171 from nucleotide 913 to nucleotide 1449, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:171 from nucleotide 913 to nucleotide 1449.

In other embodiments, the present invention provides a composition comprising
5 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:172;
- (b) a fragment of the amino acid sequence of SEQ ID NO:172, the fragment comprising eight contiguous amino acids of SEQ ID NO:172; and
- 10 (c) the amino acid sequence encoded by the cDNA insert of clone fx317_11 deposited with the ATCC under accession number 98663;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:172. In further preferred
15 amino acid sequence of SEQ ID NO:172 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:172, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment comprising the amino acid sequence from amino acid 205 to amino acid 214 of SEQ ID NO:172.

20 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:173;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:173 from nucleotide 51 to nucleotide 1202;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone lp547_4 deposited with the ATCC under accession number 98663;
- (d) a polynucleotide encoding the full-length protein encoded by the
30 cDNA insert of clone lp547_4 deposited with the ATCC under accession number 98663;

- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone lp547_4 deposited with the ATCC under accession number 98663;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone lp547_4 deposited with the ATCC under accession number 98663;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:174;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:174;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:173.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:173 from nucleotide 51 to nucleotide 1202; the nucleotide sequence of the full-length protein coding sequence of clone lp547_4 deposited with the ATCC under accession number 98663; or the nucleotide sequence of a mature protein coding sequence of clone lp547_4 deposited with the ATCC under accession number 98663. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone lp547_4 deposited with the ATCC under accession number 98663. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:174, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment comprising the amino acid sequence from amino acid 187 to amino acid 196 of SEQ ID NO:174.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:173.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:173, but excluding the poly(A) tail at the
- 10 3' end of SEQ ID NO:173; and
- (ab) the nucleotide sequence of the cDNA insert of clone lp547_4 deposited with the ATCC under accession number 98663;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:173, but excluding the poly(A) tail at the 3' end of SEQ ID NO:173; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 lp547_4 deposited with the ATCC under accession number 98663;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:173 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:173, but

excluding the poly(A) tail at the 3' end of SEQ ID NO:173. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173 from nucleotide 51 to nucleotide 1202, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:173 from nucleotide 51 to nucleotide 1202, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:173 from nucleotide 51 to nucleotide 1202.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:174;
- (b) a fragment of the amino acid sequence of SEQ ID NO:174, the fragment comprising eight contiguous amino acids of SEQ ID NO:174; and
- (c) the amino acid sequence encoded by the cDNA insert of clone lp547_4 deposited with the ATCC under accession number 98663;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:174. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:174, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment comprising the amino acid sequence from amino acid 187 to amino acid 196 of SEQ ID NO:174.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175 from nucleotide 61 to nucleotide 2559;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175 from nucleotide 904 to nucleotide 2559;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone lv310_7 deposited with the ATCC under accession number 98663;

5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone lv310_7 deposited with the ATCC under accession number 98663;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone lv310_7 deposited with the ATCC under accession number 98663;

10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone lv310_7 deposited with the ATCC under accession number 98663;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:176;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:176;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:175.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:175 from nucleotide 61 to nucleotide 2559; the nucleotide sequence of SEQ ID NO:175 from nucleotide 904 to nucleotide 2559; the nucleotide sequence of the full-length protein coding sequence of clone lv310_7 deposited with the ATCC under accession number 98663; or the nucleotide sequence of a mature protein coding sequence of clone lv310_7 deposited with the ATCC under accession number 98663. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone lv310_7 deposited with the ATCC under accession number

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98663. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:176, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment comprising the amino acid sequence from amino acid 411 to amino acid 420 of SEQ ID NO:176.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:175.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:175, but excluding the poly(A) tail at the 3' end of SEQ ID NO:175; and

(ab) the nucleotide sequence of the cDNA insert of clone lv310_7 deposited with the ATCC under accession number 98663;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:175, but excluding the poly(A) tail at the 3' end of SEQ ID NO:175; and

(bb) the nucleotide sequence of the cDNA insert of clone lv310_7 deposited with the ATCC under accession number 98663;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:175 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:175, but excluding the poly(A) tail at the 3' end of SEQ ID NO:175. Also preferably the
10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175 from nucleotide 61 to nucleotide 2559, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:175 from nucleotide 61 to nucleotide 2559, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:175 from nucleotide
15 61 to nucleotide 2559. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175 from nucleotide 904 to nucleotide 2559, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:175 from nucleotide 904 to nucleotide 2559, to a nucleotide sequence corresponding to the 3' end
20 of said sequence of SEQ ID NO:175 from nucleotide 904 to nucleotide 2559.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:176;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:176, the fragment comprising eight contiguous amino acids of SEQ ID NO:176; and
- (c) the amino acid sequence encoded by the cDNA insert of clone lv310_7 deposited with the ATCC under accession number 98663;

the protein being substantially free from other mammalian proteins. Preferably such
30 protein comprises the amino acid sequence of SEQ ID NO:176. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous

amino acids of SEQ ID NO:176, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment comprising the amino acid sequence from amino acid 411 to amino acid 420 of SEQ ID NO:176.

In one embodiment, the present invention provides a composition comprising an
5 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177 from nucleotide 389 to nucleotide 1330;
- 10 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177 from nucleotide 1286 to nucleotide 1330;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone nq34_12 deposited with the ATCC under accession number 98663;
- 15 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone nq34_12 deposited with the ATCC under accession number 98663;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone nq34_12 deposited with the ATCC under
20 accession number 98663;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone nq34_12 deposited with the ATCC under accession number 98663;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:178;
- 25 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:178;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 30 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:177.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:177 from nucleotide 389 to nucleotide 1330; the nucleotide sequence of SEQ ID NO:177 from nucleotide 1286 to nucleotide 1330; the nucleotide sequence of the full-length protein coding sequence of clone nq34_12 deposited with the ATCC under accession number 98663; or the nucleotide sequence of a mature protein coding sequence of clone nq34_12 deposited with the ATCC under accession number 98663. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone nq34_12 deposited with the ATCC under accession number 98663. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:178, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment comprising the amino acid sequence from amino acid 152 to amino acid 161 of SEQ ID NO:178.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:177.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:177, but excluding the poly(A) tail at the 3' end of SEQ ID NO:177; and
 - (ab) the nucleotide sequence of the cDNA insert of clone nq34_12 deposited with the ATCC under accession number 98663;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:177, but excluding the poly(A) tail at the 3' end of SEQ ID NO:177; and

10 (bb) the nucleotide sequence of the cDNA insert of clone nq34_12 deposited with the ATCC under accession number 98663;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:177 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:177, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:177. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177 from nucleotide 389 to nucleotide 1330, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:177 from nucleotide 389 to nucleotide 1330,
25 to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:177 from nucleotide 389 to nucleotide 1330. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177 from nucleotide 1286 to nucleotide 1330, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said
30 sequence of SEQ ID NO:177 from nucleotide 1286 to nucleotide 1330, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:177 from nucleotide 1286 to nucleotide 1330.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:178;
- 5 (b) a fragment of the amino acid sequence of SEQ ID NO:178, the fragment comprising eight contiguous amino acids of SEQ ID NO:178; and
- (c) the amino acid sequence encoded by the cDNA insert of clone nq34_12 deposited with the ATCC under accession number 98663;

the protein being substantially free from other mammalian proteins. Preferably such
10 protein comprises the amino acid sequence of SEQ ID NO:178. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous
15 amino acids of SEQ ID NO:178, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment comprising the amino acid sequence from amino acid 152 to amino acid 161 of SEQ ID NO:178.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
20 NO:179;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179 from nucleotide 1026 to nucleotide 1226;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179 from nucleotide 1101 to nucleotide 1226;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pj154_1 deposited with the ATCC under accession number 98663;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pj154_1 deposited with the ATCC under accession number
30 98663;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pj154_1 deposited with the ATCC under accession number 98663;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pj154_1 deposited with the ATCC under accession number 98663;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:180;

5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:180;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any
15 one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:179.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:179 from nucleotide 1026 to nucleotide 1226; the nucleotide sequence of SEQ ID NO:179 from nucleotide 1101 to nucleotide 1226; the nucleotide sequence of the full-
20 length protein coding sequence of clone pj154_1 deposited with the ATCC under accession number 98663; or the nucleotide sequence of a mature protein coding sequence of clone pj154_1 deposited with the ATCC under accession number 98663. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pj154_1 deposited with the ATCC under accession
25 number 98663. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:180, or a polynucleotide encoding a protein comprising a fragment of the amino acid
30 sequence of SEQ ID NO:180 having biological activity, the fragment comprising the amino acid sequence from amino acid 28 to amino acid 37 of SEQ ID NO:180.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:179.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

5 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:179, but excluding the poly(A) tail at the 3' end of SEQ ID NO:179; and

10 (ab) the nucleotide sequence of the cDNA insert of clone pj154_1 deposited with the ATCC under accession number 98663;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

15 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (ba) SEQ ID NO:179, but excluding the poly(A) tail at the 3' end of SEQ ID NO:179; and

(bb) the nucleotide sequence of the cDNA insert of clone pj154_1 deposited with the ATCC under accession number 98663;

25 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:179, and
30 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:179 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:179, but excluding the poly(A) tail at the 3' end of SEQ ID NO:179. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the cDNA sequence of SEQ ID NO:179 from nucleotide 1026 to nucleotide 1226, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:179 from nucleotide 1026 to nucleotide 1226, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:179
5 from nucleotide 1026 to nucleotide 1226. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:179 from nucleotide 1101 to nucleotide 1226, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:179 from nucleotide 1101 to nucleotide 1226, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:179 from nucleotide 1101 to nucleotide 1226.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:180;
- (b) a fragment of the amino acid sequence of SEQ ID NO:180, the fragment comprising eight contiguous amino acids of SEQ ID NO:180; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pj154_1 deposited with the ATCC under accession number 98663;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:180. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous
25 amino acids of SEQ ID NO:180, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment comprising the amino acid sequence from amino acid 28 to amino acid 37 of SEQ ID NO:180.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:181;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:181 from nucleotide 478 to nucleotide 651;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:181 from nucleotide 562 to nucleotide 651;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pk147_1 deposited with the ATCC under accession number 98663;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pk147_1 deposited with the ATCC under accession number 98663;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pk147_1 deposited with the ATCC under accession number 98663;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pk147_1 deposited with the ATCC under accession number 98663;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:182;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:182;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:181.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:181 from nucleotide 478 to nucleotide 651; the nucleotide sequence of SEQ ID NO:181 from nucleotide 562 to nucleotide 651; the nucleotide sequence of the full-length protein coding sequence of clone pk147_1 deposited with the ATCC under accession number 98663; or the nucleotide sequence of a mature protein coding sequence of clone pk147_1 deposited with the ATCC under accession number 98663. In other preferred

embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pk147_1 deposited with the ATCC under accession number 98663. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:182, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:182.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:181.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:181, but excluding the poly(A) tail at the 3' end of SEQ ID NO:181; and

(ab) the nucleotide sequence of the cDNA insert of clone pk147_1 deposited with the ATCC under accession number 98663;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:181, but excluding the poly(A) tail at the 3' end of SEQ ID NO:181; and

- (bb) the nucleotide sequence of the cDNA insert of clone pk147_1 deposited with the ATCC under accession number 98663;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:181, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:181 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:181, but excluding the poly(A) tail at the 3' end of SEQ ID NO:181. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:181 from nucleotide 478 to nucleotide 651, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:181 from nucleotide 478 to nucleotide 651, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:181 from nucleotide 478 to nucleotide 651. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:181 from nucleotide 562 to nucleotide 651, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:181 from nucleotide 562 to nucleotide 651, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:181 from nucleotide 562 to nucleotide 651.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:182;
- (b) a fragment of the amino acid sequence of SEQ ID NO:182, the fragment comprising eight contiguous amino acids of SEQ ID NO:182; and
- 30 (c) the amino acid sequence encoded by the cDNA insert of clone pk147_1 deposited with the ATCC under accession number 98663;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:182. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:182, or a protein comprising a fragment of the amino acid
5 sequence of SEQ ID NO:182 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:182.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:183;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:183 from nucleotide 1129 to nucleotide 1896;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:183 from nucleotide 1189 to nucleotide 1896;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pt127_1 deposited with the ATCC under accession number 98663;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pt127_1 deposited with the ATCC under accession number
20 98663;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pt127_1 deposited with the ATCC under accession number 98663;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
25 insert of clone pt127_1 deposited with the ATCC under accession number 98663;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:184;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment
30 comprising eight contiguous amino acids of SEQ ID NO:184;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

5 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:183.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:183 from nucleotide 1129 to nucleotide 1896; the nucleotide sequence of SEQ ID NO:183 from nucleotide 1189 to nucleotide 1896; the nucleotide sequence of the full-length protein coding sequence of clone pt127_1 deposited with the ATCC under
10 accession number 98663; or the nucleotide sequence of a mature protein coding sequence of clone pt127_1 deposited with the ATCC under accession number 98663. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein
15 encoded by the cDNA insert of clone pt127_1 deposited with the ATCC under accession number 98663. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment preferably comprising eight
(more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID
20 NO:184, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment comprising the amino acid sequence from amino acid 123 to amino acid 132 of SEQ ID NO:184.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:183.

25 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
30 consisting of:

(aa) SEQ ID NO:183, but excluding the poly(A) tail at the 3' end of SEQ ID NO:183; and

- (ab) the nucleotide sequence of the cDNA insert of clone pt127_1 deposited with the ATCC under accession number 98663;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:183, but excluding the poly(A) tail at the 3' end of SEQ ID NO:183; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 pt127_1 deposited with the ATCC under accession number 98663;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:183, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:183 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:183, but excluding the poly(A) tail at the 3' end of SEQ ID NO:183. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:183 from nucleotide 1129 to nucleotide 1896, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:183 from nucleotide 1129 to nucleotide 1896, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:183
- 30 from nucleotide 1129 to nucleotide 1896. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:183 from nucleotide 1189 to nucleotide 1896, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said

sequence of SEQ ID NO:183 from nucleotide 1189 to nucleotide 1896, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:183 from nucleotide 1189 to nucleotide 1896.

In other embodiments, the present invention provides a composition comprising
5 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:184;
- (b) a fragment of the amino acid sequence of SEQ ID NO:184, the fragment comprising eight contiguous amino acids of SEQ ID NO:184; and
- 10 (c) the amino acid sequence encoded by the cDNA insert of clone pt127_1 deposited with the ATCC under accession number 98663;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:184. In further preferred
15 amino acid sequence of SEQ ID NO:184 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:184, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment comprising the amino acid sequence from amino acid 123 to amino acid 132 of SEQ ID NO:184.

20 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:185;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:185 from nucleotide 172 to nucleotide 1041;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:185 from nucleotide 295 to nucleotide 1041;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qo115_13 deposited with the ATCC under
30 accession number 98663;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qo115_13 deposited with the ATCC under accession number 98663;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qo115_13 deposited with the ATCC under accession number 98663;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qo115_13 deposited with the ATCC under accession number 98663;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:186;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:186;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:185.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:185 from nucleotide 172 to nucleotide 1041; the nucleotide sequence of SEQ ID NO:185 from nucleotide 295 to nucleotide 1041; the nucleotide sequence of the full-length protein coding sequence of clone qo115_13 deposited with the ATCC under accession number 98663; or the nucleotide sequence of a mature protein coding sequence of clone qo115_13 deposited with the ATCC under accession number 98663. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qo115_13 deposited with the ATCC under accession number 98663. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:186, or a polynucleotide encoding a protein comprising a fragment of the amino acid

sequence of SEQ ID NO:186 having biological activity, the fragment comprising the amino acid sequence from amino acid 140 to amino acid 149 of SEQ ID NO:186.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:185.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:185, but excluding the poly(A) tail at the 3' end of SEQ ID NO:185; and

15 (ab) the nucleotide sequence of the cDNA insert of clone qo115_13 deposited with the ATCC under accession number 98663;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

20 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:185, but excluding the poly(A) tail at the 3' end of SEQ ID NO:185; and

(bb) the nucleotide sequence of the cDNA insert of clone qo115_13 deposited with the ATCC under accession number 98663;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:185, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:185 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:185, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:185. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:185 from nucleotide 172 to nucleotide 1041, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:185 from nucleotide 172 to nucleotide 1041,
10 to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:185 from nucleotide 172 to nucleotide 1041. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:185 from nucleotide 295 to nucleotide 1041, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of
15 SEQ ID NO:185 from nucleotide 295 to nucleotide 1041, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:185 from nucleotide 295 to nucleotide 1041.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the
20 group consisting of:

- (a) the amino acid sequence of SEQ ID NO:186;
- (b) a fragment of the amino acid sequence of SEQ ID NO:186, the fragment comprising eight contiguous amino acids of SEQ ID NO:186; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
25 qo115_13 deposited with the ATCC under accession number 98663;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:186. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment
30 preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:186, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment comprising the amino acid sequence from amino acid 140 to amino acid 149 of SEQ ID NO:186.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial, yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the present invention are organisms that have enhanced, reduced, or
5 modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

- (a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and
- 10 (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which
15 specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

20

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

25

DETAILED DESCRIPTION

ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone
30 in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its

sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Clone "bd306_7"

A polynucleotide of the present invention has been identified as clone "bd306_7". bd306_7 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bd306_7 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bd306_7 protein").

The nucleotide sequence of bd306_7 as presently determined is reported in SEQ ID NO:1, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bd306_7 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2. Amino acids 11 to 23 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the bd306_7 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bd306_7 should be approximately 3700 bp.

The nucleotide sequence disclosed herein for bd306_7 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bd306_7 demonstrated at least some similarity with sequences

identified as AA027096 (zk04d03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469541 3'), AA027135 (zk04d03.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469541 5'), AA166312 (ms42g11.r1 Life Tech mouse embryo 135dpc 10666014 Mus musculus cDNA clone 6142765' similar to TRE238793 E238793 DUALIN), AA535890 (nf94a03.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:927532), H14467 (yl25g07.r1 Homo sapiens cDNA clone 159324 5' similar to contains HGR repetitive element), T21281 (Human gene signature HUMGS02637), T61016 (Total DNA sequence from cosmid clones LP(2)127 and LP(2)128), U47621 (Human nucleolar autoantigen No55 mRNA, complete cds), W51808 (zc48g04.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 325590 5' similar to PIR:S20742 S20742 synaptonemal complex protein Sc65 - rat; contains Alu repetitive element; mRNA sequence), and X97607 (G.gallus mRNA for cartilage associated protein). The predicted amino acid sequence disclosed herein for bd306_7 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bd306_7 protein demonstrated at least some similarity to sequences identified as R95913 (Neural thread protein [Homo sapiens]), U47621 (nucleolar autoantigen No55 [Homo sapiens]), and X97607 (cartilage associated protein [Gallus gallus]). Two regions of bd306_7 protein (amino acids 148-217 and 298-367 of SEQ ID NO:2) align with the same region, amino acids 145-214, of cartilage associated protein. The homology between bd306_7 protein and nucleolar autoantigen No55 is also good, but in this case it appears that bd306_7 amino acids 148-189 is similar to two regions of No55 (amino acids 145-186 and 296-337), and bd306_7 amino acids 298-367 are also similar to nearly the same two regions of No55 (amino acids 145-214 and 296-365). This implies that two regions in bd306_7 (roughly 148-189 and 298-367) are similar to each other, and one copy of this region is found in cartilage associated protein, but both are present in No55. Cartilage associated protein is reported to be localized to the extracellular matrix [J. Cell Sci 1997 110(Pt 12):1351-1359], while No55 is found in the granular component of the nucleolus [Mol Biol Cell 1996 7(7):1015-1024]. Based upon sequence similarity, bd306_7 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of bd306_7 also indicates that it may contain an Alu repetitive element.

bd306_7 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 52 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "fj283_11" and Clone "fj283_6"

Polynucleotides of the present invention have been identified as clone "fj283_11" and clone "fj283_6". fj283_11 and fj283_6 were isolated from a human adult lung carcinoma cDNA library using methods which are selective for cDNAs encoding secreted
5 proteins (see U.S. Pat. No. 5,536,637), or were identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fj283_11 and fj283_6 are full-length clones, including the entire coding sequence of a secreted protein (also referred to herein as "fj283 protein").

The nucleotide sequence of fj283_11 as presently determined is reported in SEQ
10 ID NO:3, and includes a poly(A) tail. The nucleotide sequence of fj283_6 as presently determined is reported in SEQ ID NO:198, and includes a poly(A) tail. Although cDNA clones fj283_11 and fj283_6 have different nucleotide sequences, perhaps as a result of alternative splicing of a common primary mRNA transcript (particularly between nucleotide 402 and nucleotide 618 of SEQ ID NO:198), these clones are predicted to
15 encode the same protein. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the fj283 protein corresponding to the foregoing nucleotide sequences is reported in SEQ ID NO:4. Amino acids 8 to 20 of SEQ ID NO:4 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of the predicted
20 leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the fj283 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fj283_11 should be approximately 3350 bp. The EcoRI/NotI restriction fragment
25 obtainable from the deposit containing clone fj283_6 should be approximately 2700 bp.

The nucleotide sequences disclosed herein for fj283_11 and fj283_6 were searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fj283_11 and/or fj283_6 demonstrated at least some similarity with sequences identified as AA052962 (zl70c02.s1 Stratagene
30 colon (#937204) Homo sapiens cDNA clone 509954 3' similar to gb D14531 60S RIBOSOMAL PROTEIN L9 (HUMAN)), AA080949 (zn04d12.r1 Stratagene hNT), AA160948 (zq40e12.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 632206 5'), AA195089 (zr34c02.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 665282

5', mRNA sequence), AA258887 (zs32b02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686859 5'), H97993 (yw06e03.s1 Homo sapiens cDNA clone 251452 3'), R19768 (yg40g06.r1 Homo sapiens cDNA clone 34951 5'), U09953 (Human ribosomal protein L9 mRNA, complete cds), Z73639 (Human DNA sequence from cosmid V389H8 on chromosome X; Contains mRNA near btk gene involved in a-gamma-globulinemia, ESTs, STS), and Z73901 (Human DNA sequence from cosmid V389H8, between markers DXS366 and DXS87 on chromosome X contains pseudogene, mRNA near btk gene involved in a-gamma-globulinemia, ESTs, STSs). The predicted amino acid sequence disclosed herein for the fj283 protein was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted fj283 protein demonstrated at least some similarity to sequences identified as AB011084 (KIAA0512 protein [Homo sapiens]) and U09953 (ribosomal protein L9 [Homo sapiens]). Based upon sequence similarity, fj283 proteins and each similar protein or peptide may share at least some activity. Profile hidden markov model analysis has revealed the presence of an Armadillo/beta-catenin-like domain within the predicted fj283 protein sequence. The armadillo multigene family comprises many proteins widely differing in sizes and functions which have in common a variable number of tandemly repeated arm sequences of about 42 amino acids in length. Many, but not all, armadillo-repeat-containing proteins are nuclear in localization. The predicted fj283 protein does not appear to be of the nuclear variety, but rather appears to be an extracellular protein.

Clone "fk317_3"

A polynucleotide of the present invention has been identified as clone "fk317_3". fk317_3 was isolated from a human adult kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fk317_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "fk317_3 protein").

The nucleotide sequence of fk317_3 as presently determined is reported in SEQ ID NO:5, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the fk317_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fk317_3 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for fk317_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fk317_3 demonstrated at least some similarity with sequences identified as AA568588 (nm21b11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1060797), AC002326 (Genomic sequence from Human 6, complete sequence), H48562 (yq78g07.s1 Homo sapiens cDNA clone 201948 3' similar to contains Alu repetitive element; contains MER30 repetitive element), T67164 (Human alpha-N-acetylglucosaminidase gene), and Z46941 (H.sapiens DNA for alu repeats). The predicted amino acid sequence disclosed herein for fk317_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted fk317_3 protein demonstrated at least some similarity to sequences identified as X55777 (put. ORF [Homo sapiens]). Based upon sequence similarity, fk317_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the fk317_3 protein sequence centered around amino acid 42 of SEQ ID NO:6. The nucleotide sequence of fk317_3 indicates that it may contain an Alu repetitive element.

Clone "k213_2x"

A polynucleotide of the present invention has been identified as clone "k213_2x". Secreted cDNA clones were first isolated from a murine adult bone marrow (stromal cell line FCM-4) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or were identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. These murine cDNAs were then used to isolate k213_2x, a full-length human cDNA clone, including the entire coding sequence of a secreted protein (also referred to herein as "k213_2x protein").

The nucleotide sequence of k213_2x as presently determined is reported in SEQ ID NO:7, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the k213_2x protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:8. Amino acids 26 to 38 are a predicted leader/signal sequence, with the predicted mature amino

acid sequence beginning at amino acid 39. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the k213_2x protein.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone k213_2x should be approximately 1900 bp.

 The nucleotide sequence disclosed herein for k213_2x was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. k213_2x demonstrated at least some similarity with sequences
10 identified as AA123852 (mp96e08.r1 Soares 2NbMT Mus musculus cDNA clone 577094 5'), AA362005 (EST71348 T-cell lymphoma Homo sapiens cDNA 5' end), AA436477 (zv08f05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 753057 3'), AA436528 (zv08f05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753057 5'), AA643506 (nq86f04.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1159231, mRNA
15 sequence), F13485 (H. sapiens partial cDNA sequence; clone c-3dh08), and T19502 (Human gene signature HUMGS00560). Based upon sequence similarity, k213_2x proteins and each similar protein or peptide may share at least some activity.

 k213_2x protein was expressed in a COS cell expression system, and an expressed protein band of approximately 6 kDa was detected in membrane fractions using SDS
20 polyacrylamide gel electrophoresis.

Clone "na316_1"

 A polynucleotide of the present invention has been identified as clone "na316_1". na316_1 was isolated from a human adult brain (corpus callosum) cDNA library using
25 methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. na316_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "na316_1 protein").

30 The nucleotide sequence of na316_1 as presently determined is reported in SEQ ID NO:9, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the na316_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10. Amino

acids 30 to 42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 43. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the na316_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone na316_1 should be approximately 900 bp.

The nucleotide sequence disclosed herein for na316_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database. The TopPredII computer program predicts two potential transmembrane domains within the na316_1 protein sequence, centered around amino acids 31 and 66 of SEQ ID NO:10, respectively.

Clone "nf93_20"

A polynucleotide of the present invention has been identified as clone "nf93_20". nf93_20 was isolated from a human adult brain (substantia nigra) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. nf93_20 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "nf93_20 protein").

The nucleotide sequence of nf93_20 as presently determined is reported in SEQ ID NO:11, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the nf93_20 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:12. Amino acids 6 to 18 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the nf93_20 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone nf93_20 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for nf93_20 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. nf93_20 demonstrated at least some similarity with sequences identified as AA063620 (ze87g07.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 366012 3'), AA317410 (EST19337 Retina II Homo sapiens cDNA 5' end), H29417 (ym60e07.r1 Homo sapiens cDNA clone 52631 5'), and N41425 (yw93e08.r1 Homo sapiens cDNA clone 259814 5'). Based upon sequence similarity, nf93_20 proteins and each similar protein or peptide may share at least some activity.

nf93_20 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 29 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "np164_1"

A polynucleotide of the present invention has been identified as clone "np164_1". np164_1 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. np164_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "np164_1 protein").

The nucleotide sequence of np164_1 as presently determined is reported in SEQ ID NO:13, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the np164_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14. Amino acids 348 to 360 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 361. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the np164_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone np164_1 should be approximately 2100 bp.

The nucleotide sequence disclosed herein for np164_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. np164_1 demonstrated at least some similarity with sequences identified as N63143 (yz37c12.s1 Homo sapiens cDNA clone 285238 3'), T19992 (Human gene signature HUMGS01129), Z46676 (Caenorhabditis elegans cosmid C08B11, complete sequence), and Z74910 (S.cerevisiae chromosome XV reading frame ORF YOR002w). The
5 predicted amino acid sequence disclosed herein for np164_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted np164_1 protein demonstrated at least some similarity to sequences identified as Z46676 (C08B11.8 [Caenorhabditis elegans]) and Z74910 (ORF YOR002w [Saccharomyces cerevisiae]). Based upon sequence similarity, np164_1 proteins and each
10 similar protein or peptide may share at least some activity. The TopPredII computer program predicts ten potential transmembrane domains within the np164_1 protein sequence, centered around amino acids 4, 114, 165, 229, 293, 322, 360, 386, 436, and 465 of SEQ ID NO:14, respectively.

np164_1 protein was expressed in a COS cell expression system, and an expressed
15 protein band of approximately 43 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "pe204_1"

A polynucleotide of the present invention has been identified as clone "pe204_1".
20 pe204_1 was isolated from a human adult blood (chronic myelogenous leukemia K5) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pe204_1 is a full-length clone, including the entire coding sequence of a secreted
25 protein (also referred to herein as "pe204_1 protein").

The nucleotide sequence of pe204_1 as presently determined is reported in SEQ ID NO:15, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pe204_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16. Amino
30 acids 116 to 128 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 129. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should

the predicted leader/signal sequence not be separated from the remainder of the pe204_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pe204_1 should be approximately 1100 bp.

5 The nucleotide sequence disclosed herein for pe204_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pe204_1 demonstrated at least some similarity with sequences identified as AA279961 (zs92h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 704991 3'), AA306911 (EST178043 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end),
10 AC002086 (Human PAC clone DJ525N14), AC002094 (Genomic sequence from Human 17, complete sequence), T97749 (ye58c04.s1 Homo sapiens cDNA clone), Z74696 (Human DNA sequence from cosmid 203C2, between markers DXS6791 and DXS8038 on chromosome X contains ESTs), Z80901 (Human DNA sequence from cosmid N119A7 on chromosome 22q12-qter), and Z82245 (Human DNA sequence *** SEQUENCING IN
15 PROGRESS *** from clone 799F10; HTGS phase 1). The predicted amino acid sequence disclosed herein for pe204_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pe204_1 protein demonstrated at least some similarity to sequences identified as K02113 (Gallus gallus vitellogenin [Gallus gallus]). Based upon sequence similarity, pe204_1 proteins and each
20 similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the pe204_1 protein sequence, one centered around amino acid 50 and another around amino acid 90 of SEQ ID NO:16.

pe204_1 protein was expressed in a COS cell expression system, and an expressed
25 protein band of approximately 14 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "ya1_1"

A polynucleotide of the present invention has been identified as clone "ya1_1".
30 ya1_1 was isolated from a human adult testes cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ya1_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ya1_1 protein").

The nucleotide sequence of ya1_1 as presently determined is reported in SEQ ID NO:17, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ya1_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:18. Amino acids 330 to 342 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 343. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ya1_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ya1_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for ya1_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ya1_1 demonstrated at least some similarity with sequences identified as AA431507 (zw76e05.r1 Soares testis NHT Homo sapiens cDNA clone 782144 5') and F03332 (H. sapiens partial cDNA sequence; clone c-1tg07). Based upon sequence similarity, ya1_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the ya1_1 protein sequence centered around amino acid 156 and around amino acid 332 of SEQ ID NO:18, respectively. The nucleotide sequence of ya1_1 indicates that it may contain an Alu repetitive element.

ya1_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 38 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "yb8_1"

A polynucleotide of the present invention has been identified as clone "yb8_1". yb8_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb8_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb8_1 protein").

The nucleotide sequence of yb8_1 as presently determined is reported in SEQ ID NO:19, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the yb8_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:20. Amino acids 69 to 81 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 82. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yb8_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb8_1 should be approximately 1800 bp.

10 The nucleotide sequence disclosed herein for yb8_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb8_1 demonstrated at least some similarity with sequences identified as AA418057 (zv97a06.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 767698 5' similar to TR:G1143719 G1143719 RS-REX-B), L10334 (Homo sapiens neuroendocrine-specific protein B (NSP) mRNA, complete cds), U17603 (Rattus norvegicus rS-Rex-s mRNA, complete cds), and W19986 (zb38e09.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 305896 5', mRNA sequence). The predicted amino acid sequence disclosed herein for yb8_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yb8_1 protein demonstrated at least some similarity to sequences identified as L10334 (neuroendocrine-specific proteins B and C [Homo sapiens]) and U17603 (rS-Rex-s [Rattus norvegicus]). Based upon sequence similarity, yb8_1 proteins and each similar protein or peptide may share at least some activity. The predicted yb8_1 protein shows significant (60% identity) amino acid similarity to the neuro-endocrine specific protein (NSP) family of proteins. Roebroek *et al.* (1993, *J. Biol. Chem.* 268: 13439, which is incorporated by reference herein) report observing three transcripts from this gene family: NSP-A (3.4 kb), -B (2.3 kb), and -C (1.8 kb); they encode proteins of 776, 356, and 208 amino acids, respectively. Roebroek *et al.* also observe that these three transcripts are identical at the 3' end and only differ over a short portion near their 5' ends, and are thus possible splice variants. NSP-A and NSP-C were found in neural and endocrine tissues while NSP-B was found only in a lung carcinoma cell line (Roebrek *et al.* state that NSP-B is "aberrant" suggesting that it might be an artifact). The C-terminal portions of the protein sequences from all three transcripts are identical. The predicted yb8_1 protein shows

strong amino acid similarity within this region and is about as long as NSP-C. Thus the predicted yb8_1 protein appears to be related to NSP-C. The TopPredII computer program predicts two potential transmembrane domains within the yb8_1 protein sequence, centered around amino acids 82 and 174 of SEQ ID NO:20, respectively.

- 5 yb8_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 25 kDa was detected in membrane fractions and in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "am856_3"

- 10 A polynucleotide of the present invention has been identified as clone "am856_3". am856_3 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. am856_3 is a full-length
15 clone, including the entire coding sequence of a secreted protein (also referred to herein as "am856_3 protein").

- The nucleotide sequence of am856_3 as presently determined is reported in SEQ ID NO:21, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the am856_3 protein
20 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:22. Amino acids 23 to 35 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 36. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the am856_3
25 protein. The amino acid sequence of another protein that could be encoded by basepairs 214 to 369 of SEQ ID NO:21 is reported in SEQ ID NO:274.

 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone am856_3 should be approximately 2100 bp.

- The nucleotide sequence disclosed herein for am856_3 was searched against the
30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. am856_3 demonstrated at least some similarity with sequences identified as M26434 (Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds), N71723 (yw52b09.r1 Homo sapiens cDNA clone 255833 5' similar to

gb | M87920 | HUMALNE652 Human carcinoma cell-derived Alu RNA transcript, (rRNA);
gb X77738_ma1 BAND 3 ANION TRANSPORT PROTEIN), U41196 (Human (TTTC)5
short tandem repeat polymorphism UM69, D17S1339), and X89398 (H.sapiens ung gene
for uracil DNA-glycosylase). Based upon sequence similarity, am856_3 proteins and each
5 similar protein or peptide may share at least some activity. The TopPredII computer
program predicts the amino-terminal half of the am856_3 protein sequence to be highly
hydrophobic. The nucleotide sequence of am856_3 indicates that it may contain one or
more of the following types of repetitive elements: AT-like, (TTTC)5 short tandem repeat
polymorphism UM69.

10

Clone "am996_12"

A polynucleotide of the present invention has been identified as clone "am996_12".
am996_12 was isolated from a human fetal kidney cDNA library using methods which
are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
15 identified as encoding a secreted or transmembrane protein on the basis of computer
analysis of the amino acid sequence of the encoded protein. am996_12 is a full-length
clone, including the entire coding sequence of a secreted protein (also referred to herein
as "am996_12 protein").

The nucleotide sequence of am996_12 as presently determined is reported in SEQ
20 ID NO:23, and includes a poly(A) tail. What applicants presently believe to be the proper
reading frame and the predicted amino acid sequence of the am996_12 protein
corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:24. Amino
acids 14 to 26 are a predicted leader/signal sequence, with the predicted mature amino
acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the
25 predicted leader/signal sequence, it is likely to act as a transmembrane domain should
the predicted leader/signal sequence not be separated from the remainder of the
am996_12 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing
clone am996_12 should be approximately 1000 bp.

30 The nucleotide sequence disclosed herein for am996_12 was searched against the
GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
FASTA search protocols. No hits were found in the database. The TopPredII computer

program predicts two potential transmembrane domains within the am996_12 protein sequence, centered around amino acids 18 and 62 of SEQ ID NO:24, respectively.

Clone "cc69_1"

5 A polynucleotide of the present invention has been identified as clone "cc69_1". cc69_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cc69_1 is a full-length clone,
10 including the entire coding sequence of a secreted protein (also referred to herein as "cc69_1 protein").

The nucleotide sequence of cc69_1 as presently determined is reported in SEQ ID NO:25, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cc69_1 protein corresponding
15 to the foregoing nucleotide sequence is reported in SEQ ID NO:26.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cc69_1 should be approximately 550 bp.

The nucleotide sequence disclosed herein for cc69_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
20 FASTA search protocols. cc69_1 demonstrated at least some similarity with sequences identified as AA280712 (zs98h11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711717 5'), AA421250 (zu27b03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 739181 3'), H28886 (yp03e09.s1 Homo sapiens cDNA clone 186376 3'), and H84171 (yv87c11.r1 Homo sapiens cDNA). Based upon sequence similarity, cc69_1
25 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the cc69_1 protein sequence centered around amino acid 15 of SEQ ID NO:26.

Clone "cc162_1"

30 A polynucleotide of the present invention has been identified as clone "cc162_1". cc162_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer

analysis of the amino acid sequence of the encoded protein. cc162_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cc162_1 protein").

5 The nucleotide sequence of cc162_1 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cc162_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28. Amino acids 2 to 14 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the
10 predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cc162_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cc162_1 should be approximately 785 bp.

15 The nucleotide sequence disclosed herein for cc162_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cc162_1 demonstrated at least some similarity with sequences identified as AA369067 (EST80419 Placenta II Homo sapiens cDNA 5' end similar to EST containing Alu repeat), L05367 (Human oligodendrocyte myelin glycoprotein (OMG)
20 exons), and R97898 (yq60b11.r1 Homo sapiens cDNA clone 200157 5'). Based upon sequence similarity, cc162_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of cc162_1 indicates that it may contain one or more of the following types of repetitive elements: ALU, L1.

25 Clone "if87_1"

A polynucleotide of the present invention has been identified as clone "if87_1". if87_1 was isolated from a human adult uterus cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
30 analysis of the amino acid sequence of the encoded protein. if87_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "if87_1 protein").

The nucleotide sequence of if87_1 as presently determined is reported in SEQ ID NO:29, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the if87_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:30. Amino acids 8 to 20
5 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the if87_1 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone if87_1 should be approximately 900 bp.

The nucleotide sequence disclosed herein for if87_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. if87_1 demonstrated at least some similarity with sequences
15 identified as AA172949 (ms20b07.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone 607477 5'), AC002310 (Homo sapiens Chromosome 16 BAC clone CIT987-SKA-635H12 ~complete genomic sequence, complete sequence), AC003012 (Human PAC clone DJ0169K13, complete sequence), D59442 (Human fetal brain cDNA 3'-end GEN-037G12), R72810 (yl09f12.r1 Homo sapiens cDNA clone 157775 5' similar to
20 contains MSR1 repetitive element), and X74358 (P.carnea Pod-EPPT mRNA). The predicted amino acid sequence disclosed herein for if87_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted if87_1 protein demonstrated at least some similarity to sequences identified as Z46970 (secreted acid phosphatase 2 (SAP2) [Leishmania mexicana]). Based upon
25 sequence similarity, if87_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the if87_1 protein sequence centered around amino acid 58 of SEQ ID NO:30. The nucleotide sequence of if87_1 indicates that it may contain one or more of the following repetitive elements: ALU, LIMA.

30 if87_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 35 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "nn103_4"

A polynucleotide of the present invention has been identified as clone "nn103_4". nn103_4 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. nn103_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "nn103_4 protein").

The nucleotide sequence of nn103_4 as presently determined is reported in SEQ ID NO:31, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the nn103_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:32. Amino acids 19 to 31 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 32. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the nn103_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone nn103_4 should be approximately 3500 bp.

The nucleotide sequence disclosed herein for nn103_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. nn103_4 demonstrated at least some similarity with sequences identified as AA134609 (zn90e04.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 565470 5'), AA584818 (no09e05.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE 1100192 similar to contains L1.t1 L1 repetitive element), AC002416 (** SEQUENCING IN PROGRESS ** Human Chromosome X; HTGS phase 1, 3 unordered pieces), AC002456 (Human BAC clone RG013L03 from 7q21, complete sequence), D25252 (Human randomly sequenced mRNA), Q05615 (Insert from pARC 1153), U95743 (Homo sapiens chromosome 16 BAC clone CIT987-SK65D3, complete sequence), Z22970 (H.sapiens mRNA for M130 antigen cytoplasmic variant 2), Z71182 (Human DNA sequence from pac 248J6, between markers DXS366 and DXS87 on chromosome X contains STS), Z81310 (Human DNA sequence from cosmid O19A on chromosome 6 Contains HLA DNA gene and STS), Z82253 (Human DNA sequence ** SEQUENCING

IN PROGRESS *** from clone U151E3; HTGS phase 1), and Z92547 (Human DNA sequence from PAC 863K). The predicted amino acid sequence disclosed herein for nn103_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted nn103_4 protein demonstrated at least
5 some similarity to sequences identified as X52235 (ORFII [Homo sapiens]). Based upon sequence similarity, nn103_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the nn103_4 protein sequence centered around amino acid 52 of SEQ ID NO:32. The nucleotide sequence of nn103_4 indicates that it may contain
10 one or more of the following types of repetitive elements: L1, A, MER31.

Clone "np206_8"

A polynucleotide of the present invention has been identified as clone "np206_8". np206_8 was isolated from a human fetal kidney (293 cell line) cDNA library using
15 methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. np206_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "np206_8 protein").

20 The nucleotide sequence of np206_8 as presently determined is reported in SEQ ID NO:33, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the np206_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:34.

The EcoRI/NotI restriction fragment obtainable from the deposit containing
25 clone np206_8 should be approximately 1900 bp.

The nucleotide sequence disclosed herein for np206_8 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. np206_8 demonstrated at least some similarity with sequences identified as AA126810 (zn87a12.r1 Stratagene lung cDNA), AC000053 (***)
30 SEQUENCING IN PROGRESS *** Human Cosmid Clone 81a12 and 70g8; HTGS phase 2), AC002094 (Genomic sequence from Human 17, complete sequence), AC002431 (Human BAC clone RG180F08 from 7q31, complete sequence), F09069 (H. sapiens partial cDNA sequence; clone c-2we10), G33587 (human STS SHGC-50493), R37071 (yf66a08.s1

Homo sapiens cDNA clone 27020 3'), U91321 (Human chromosome 16p13 BAC clone), Z68746 (Human DNA sequence from cosmid Q27, chromosome region 11p15.5), and Z92846 (Human DNA sequence from cosmid U105G4, between markers DXS366 and DXS87 on chromosome X contains ESTs). Based upon sequence similarity, np206_8
5 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of np206_8 indicates that it may contain one or more of the following types of repetitive elements: Alu/SVA.

Clone "nt746_4"

10 A polynucleotide of the present invention has been identified as clone "nt746_4". nt746_4 was isolated from a human adult brain (corpus callosum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. nt746_4 is a full-
15 length clone, including the entire coding sequence of a secreted protein (also referred to herein as "nt746_4 protein").

The nucleotide sequence of nt746_4 as presently determined is reported in SEQ ID NO:35, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the nt746_4 protein
20 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:36.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone nt746_4 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for nt746_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
25 FASTA search protocols. nt746_4 demonstrated at least some similarity with sequences identified as AA489740 (aa43c06.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 823690 5'), J04989 (Bovine alpha 1-3 galactosyltransferase mRNA completed cds), M60263 (Human alpha-1,3-galactosyltransferase (HGT-2) pseudogene), Q74712 (Galactosyl transferase clone), R24770 (yg42c11.r1 Homo sapiens cDNA clone 35316 5' similar to SP
30 GATR_BOVIN P14769 N-ACETYLLACTOSAMINIDE ALPHA-1,3-GALACTOSYL-TRANSFERASE), and S71333 (alpha 1,3 galactosyltransferase [New World monkeys, marmoset lymphoid cell line B95.8, mRNA Partial, 1131 nt]). The predicted amino acid sequence disclosed herein for nt746_4 was searched against the GenPept and GeneSeq

amino acid sequence databases using the BLASTX search protocol. The predicted nt746_4 protein demonstrated at least some similarity to sequences identified as M26925 (galactosyltransferase (EC 2.4.1.151) [Mus musculus]), R80016 (Marmoset alpha-1,3-galactosyltransferase), S71333 (alpha 1,3 galactosyltransferase, alpha 1,3GT [New World monkeys, marmoset lymphoid cell line B95.8, Peptide, 376 aa] [Platyrrhini]), and W13639 (Murine alpha(1,3)-galactosyltransferase). Based upon sequence similarity, nt746_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the nt746_4 protein sequence centered around amino acid 15 of SEQ ID NO:36. The nucleotide sequence of nt746_4 indicates that it may contain an LTR repetitive element.

nt746_4 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 100 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

15 Clone "pe286_1"

A polynucleotide of the present invention has been identified as clone "pe286_1". pe286_1 was isolated from a human adult blood (chronic myelogenous leukemia K5) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pe286_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pe286_1 protein").

The nucleotide sequence of pe286_1 as presently determined is reported in SEQ ID NO:37, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pe286_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:38.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pe286_1 should be approximately 300 bp.

The nucleotide sequence disclosed herein for pe286_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pe286_1 demonstrated at least some similarity with sequences identified as AA588854 (no21h03.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE 1101365), L46897 (Homo sapiens (subclone 3_d9 from P1 H13) DNA sequence), and

N48057 (yy99d09.s1 Homo sapiens cDNA clone 281681 3' similar to contains element MER4 repetitive element). Based upon sequence similarity, pe286_1 proteins and each similar protein or peptide may share at least some activity.

5 Clone "yb7_1"

A polynucleotide of the present invention has been identified as clone "yb7_1". yb7_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
10 analysis of the amino acid sequence of the encoded protein. yb7_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb7_1 protein").

The nucleotide sequence of yb7_1 as presently determined is reported in SEQ ID NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper
15 reading frame and the predicted amino acid sequence of the yb7_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:40.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb7_1 should be approximately 1150 bp.

The nucleotide sequence disclosed herein for yb7_1 was searched against the
20 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb7_1 demonstrated at least some similarity with sequences identified as N99344 (IMAGE:20090 Homo sapiens cDNA clone 20090). Based upon sequence similarity, yb7_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane
25 domain within the yb7_1 protein sequence located around amino acid 52 of SEQ ID NO:40; this domain is also a potential leader/signal sequence with the mature protein beginning at or near amino acid 52 of SEQ ID NO:40.

Clone "am728_60"

30 A polynucleotide of the present invention has been identified as clone "am728_60". am728_60 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis

of computer analysis of the amino acid sequence of the encoded protein. am728_60 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "am728_60 protein").

The nucleotide sequence of am728_60 as presently determined is reported in SEQ ID NO:41. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the am728_60 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone am728_60 should be approximately 4333 bp.

The nucleotide sequence disclosed herein for am728_60 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. am728_60 demonstrated at least some similarity with sequences identified as AA446039 (zw66a08.r1 Soares testis NHT Homo sapiens cDNA clone 781142 5') and U73682 (Human meningioma-expressed antigen 11 (MEA11) mRNA, partial cds). The predicted amino acid sequence disclosed herein for am728_60 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted am728_60 protein demonstrated at least some similarity to sequences identified as U67884 (melanoma inhibitory activity/condrocyte-derived retinoic acid sensitive protein homolog [Rattus norvegicus]), U73682 (meningioma-expressed antigen 11 [Homo sapiens]), U94780 (MEA6 [Homo sapiens]), and X84707 (melanoma growth regulatory protein [Homo sapiens]). Based upon sequence similarity, am728_60 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the am728_60 protein sequence, centered around amino acids 300, 370, and 670 of SEQ ID NO:42, respectively.

When expressed in COS cells, am728_60 protein was detected in a membrane fraction from these cells as a band migrating at approximately 200 kD on a denaturing SDS polyacrylamide gel.

Clone "bf377_1"

A polynucleotide of the present invention has been identified as clone "bf377_1". bf377_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was

identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bf377_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bf377_1 protein").

5 The nucleotide sequence of bf377_1 as presently determined is reported in SEQ ID NO:43, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bf377_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:44. Amino acids 27 to 39 of SEQ ID NO:44 are a predicted leader/signal sequence, with the predicted
10 mature amino acid sequence beginning at amino acid 40. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the bf377_1 protein.

 The EcoRI/NotI restriction fragment obtainable from the deposit containing
15 clone bf377_1 should be approximately 450 bp.

 The nucleotide sequence disclosed herein for bf377_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bf377_1 demonstrated at least some similarity with sequences identified as AA559859 (nl48c05.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE
20 1043912), AA657838 (nu08b11.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1207389 similar to gb:M15990 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (HUMAN)), and R49353 (yg67e07.s1 Homo sapiens cDNA clone 38126 3' similar to contains MER22 repetitive element). Based upon sequence similarity, bf377_1 proteins and each similar protein or peptide may share at least some activity.

25

Clone "cw354_1"

 A polynucleotide of the present invention has been identified as clone "cw354_1". cw354_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
30 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cw354_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw354_1 protein").

The nucleotide sequence of cw354_1 as presently determined is reported in SEQ ID NO:45, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cw354_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:46. Amino acids 28 to 40 of SEQ ID NO:46 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 41. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cw354_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw354_1 should be approximately 1350 bp.

The nucleotide sequence disclosed herein for cw354_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw354_1 demonstrated at least some similarity with sequences identified as D58859 (Human placenta cDNA 5'-end GEN-514B03), H07863 (yl86b05.s1 Homo sapiens cDNA clone 45017 3'), N32178 (yy25b09.s1 Homo sapiens cDNA clone 272249 3'), R81953 (yi98e11.r1 Homo sapiens cDNA clone 147308 5'), and W84437 (zd89d06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 356651 3'). The predicted amino acid sequence disclosed herein for cw354_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw354_1 protein demonstrated at least some similarity to sequences identified as U39726 (adenosinetriphosphatase [Mycoplasma genitalium]). Based upon sequence similarity, cw354_1 proteins and each similar protein or peptide may share at least some activity.

Clone "nm134_4"

A polynucleotide of the present invention has been identified as clone "nm134_4". nm134_4 was isolated from a human adult blood (erythroleukemia TF-1) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. nm134_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "nm134_4 protein").

The nucleotide sequence of nm134_4 as presently determined is reported in SEQ ID NO:47, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the nm134_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Amino acids 136 to 148 of SEQ ID NO:48 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 149. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the nm134_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone nm134_4 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for nm134_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. nm134_4 demonstrated at least some similarity with sequences identified as AA205020 (zq72a12.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 647134 5'), AA205286 (zq72a12.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 647134 3'), AA261864 (zs18h05.r1 Soares NbHTGBC Homo sapiens cDNA clone 685593 5'), and H63680 (yr55d03.r1 Homo sapiens cDNA clone 209189 5'). Based upon sequence similarity, nm134_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five potential transmembrane domains within the nm134_4 protein sequence centered around amino acids 108, 132, 170, 195, and 226 of SEQ ID NO:48, respectively.

Clone "yb11_1"

A polynucleotide of the present invention has been identified as clone "yb11_1". yb11_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb11_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb11_1 protein").

The nucleotide sequence of yb11_1 as presently determined is reported in SEQ ID NO:49, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb11_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:50. Amino

acids 43 to 55 of SEQ ID NO:50 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 56. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yb11_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb11_1 should be approximately 2800 bp.

The nucleotide sequence disclosed herein for yb11_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb11_1 demonstrated at least some similarity with sequences identified as R55695 (yg88f12.s1 Homo sapiens cDNA clone 40397 3') and R85100 (yo43b05.s1 Homo sapiens cDNA clone 180657 3'). Based upon sequence similarity, yb11_1 proteins and each similar protein or peptide may share at least some activity.

Clone "yc2_1"

A polynucleotide of the present invention has been identified as clone "yc2_1". yc2_1 was isolated from a human fetal kidney (293 cell line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yc2_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yc2_1 protein").

The nucleotide sequence of yc2_1 as presently determined is reported in SEQ ID NO:51, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yc2_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:52. Amino acids 15 to 27 of SEQ ID NO:52 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yc2_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yc2_1 should be approximately 2900 bp.

The nucleotide sequence disclosed herein for yc2_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yc2_1 demonstrated at least some similarity with sequences identified as AA618531 (np38a03.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone
5 IMAGE:1118572 similar to contains Alu repetitive element) and AA626937 (af84h07.s1 Soares testis NHT Homo sapiens cDNA clone 1048765 3'). Based upon sequence similarity, yc2_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of yc2_1 indicates that it may contain one or more Alu repetitive elements.

10

Clone "ff168_12"

A polynucleotide of the present invention has been identified as clone "ff168_12". ff168_12 was isolated from a human adult testes (teratocarcinoma NCCIT) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat.
15 No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ff168_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ff168_12 protein").

The nucleotide sequence of ff168_12 as presently determined is reported in SEQ
20 ID NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ff168_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:54.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ff168_12 should be approximately 1600 bp.

25 The nucleotide sequence disclosed herein for ff168_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ff168_12 demonstrated at least some similarity with sequences identified as AA025945 (ze91e02.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 366362 5'), AA156237 (zl50c09.s1 Soares pregnant uterus NbHPU Homo sapiens
30 cDNA clone 505360 3'), AA420993 (zu08e09.s1 Soares testis NHT Homo sapiens cDNA clone 731272 3'), N78486 (yz78e03.r1 Homo sapiens cDNA clone 289180 5'), W01843 (za80a01.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 298824 5'), and W95777 (ze07e02.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358298 5').

Based upon sequence similarity, ff168_12 proteins and each similar protein or peptide may share at least some activity.

Clone "ls9_1"

5 A polynucleotide of the present invention has been identified as clone "ls9_1". ls9_1 was isolated from a human adult brain (substantia nigra) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ls9_1 is a full-
10 length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ls9_1 protein").

The nucleotide sequence of ls9_1 as presently determined is reported in SEQ ID NO:55, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ls9_1 protein corresponding
15 to the foregoing nucleotide sequence is reported in SEQ ID NO:56. Amino acids 60 to 72 of SEQ ID NO:56 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 73. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ls9_1
20 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ls9_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for ls9_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
25 FASTA search protocols. ls9_1 demonstrated at least some similarity with sequences identified as AA527586 (ng42d05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937449), AC000119 (Human BAC clone RG104I04 from 7q21-7q22, complete sequence), T18551 (Human polycystic kidney disease normal PKD1 gene), Y10196 (H.sapiens PEX gene), and Z94721 (Human DNA sequence *** SEQUENCING IN
30 PROGRESS *** from clone 167A14; HTGS phase 1). The predicted amino acid sequence disclosed herein for ls9_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ls9_1 protein demonstrated at least some similarity to sequences identified as AB002375 (KIAA0377

[Homo sapiens]) and R95913 (Neural thread protein). Based upon sequence similarity, ls9_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the ls9_1 protein sequence centered around amino acid 40 of SEQ ID NO:56. The
5 nucleotide sequence of ls9_1 indicates that it may contain an Alu/SVA repetitive element.

Clone "na1010_1"

A polynucleotide of the present invention has been identified as clone "na1010_1". na1010_1 was isolated from a human adult brain cDNA library using methods which are
10 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. na1010_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "na1010_1 protein").

15 The nucleotide sequence of na1010_1 as presently determined is reported in SEQ ID NO:57, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the na1010_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:58. Amino acids 24 to 36 of SEQ ID NO:58 are a predicted leader/signal sequence, with the predicted
20 mature amino acid sequence beginning at amino acid 37. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the na1010_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing
25 clone na1010_1 should be approximately 1050 bp.

The nucleotide sequence disclosed herein for na1010_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. na1010_1 demonstrated at least some similarity with sequences identified as AC002091 (Genomic sequence from Human 17, complete sequence),
30 AC002382 (Human BAC clone RG022J17 from 7q21, complete sequence), and M26434 (Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds). Based upon sequence similarity, na1010_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of na1010_1 indicates that it may

contain one or more of the following repetitive elements: L1/A/MIR/SVA/LTRII, Alu/SVA/A/GAA, or Alu/A/GAAAA.

Clone "nf87_1"

5 A polynucleotide of the present invention has been identified as clone "nf87_1". nf87_1 was isolated from a human adult brain (substantia nigra) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. nf87_1 is a full-
10 length clone, including the entire coding sequence of a secreted protein (also referred to herein as "nf87_1 protein").

The nucleotide sequence of nf87_1 as presently determined is reported in SEQ ID NO:59, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the nf87_1 protein corresponding
15 to the foregoing nucleotide sequence is reported in SEQ ID NO:60. Amino acids 53 to 65 of SEQ ID NO:60 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 66. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the nf87_1
20 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone nf87_1 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for nf87_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
25 FASTA search protocols. nf87_1 demonstrated at least some similarity with sequences identified as AA358277 (EST67398 Fetal lung III Homo sapiens cDNA 5' end similar to similar to interferon-alpha-inducible gene p27), W52706 (zc55g02.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 326258 5' similar to SW INI7_HUMAN P40305 INTERFERON-ALPHA INDUCED 11.5 KD PROTEIN), and X67325 (H.sapiens
30 p27 mRNA). The predicted amino acid sequence disclosed herein for nf87_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted nf87_1 protein demonstrated at least some similarity to sequences identified as X67325 (p27 gene product [Homo sapiens]). The

interferon-alpha-inducible gene is localized on human chromosome 14q32 and expresses the highly hydrophobic p27 gene product in breast carcinoma cells. Based upon sequence similarity, nf87_1 proteins and each similar protein or peptide may share at least some activity.

- 5 nf87_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 16 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "nh796_1"

- 10 A polynucleotide of the present invention has been identified as clone "nh796_1". nh796_1 was isolated from a human adult brain (thalamus) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. nh796_1 is a full-
15 length clone, including the entire coding sequence of a secreted protein (also referred to herein as "nh796_1 protein").

- The nucleotide sequence of nh796_1 as presently determined is reported in SEQ ID NO:61, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the nh796_1 protein
20 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:62. Amino acids 7 to 19 of SEQ ID NO:62 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the
25 nh796_1 protein.

 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone nh796_1 should be approximately 1050 bp.

- The nucleotide sequence disclosed herein for nh796_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
30 FASTA search protocols. nh796_1 demonstrated at least some similarity with sequences identified as AA315985 (EST18772 Lung Homo sapiens cDNA 5' end), N23239 (yw47b07.s1 Homo sapiens cDNA clone 255349 3'), N27741 (yw51c06.s1 Homo sapiens cDNA clone 255754 3'), U69172 (Mus musculus unknown protein mRNA, complete cds),

and Z24371 (H. sapiens (D20S195) DNA segment containing (CA) repeat; clone AFM321xc1; single read). The predicted amino acid sequence disclosed herein for nh796_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted nh796_1 protein demonstrated at least
5 some similarity to sequences identified as U69172 (unknown [Mus musculus]). The mouse protein of unknown function (U69172) is expressed in late palate development. Based upon sequence similarity, nh796_1 proteins and each similar protein or peptide may share at least some activity.

nh796_1 protein was expressed in a COS cell expression system, and an expressed
10 protein band of approximately 25 kDa was detected in conditioned media and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "nn229_1"

A polynucleotide of the present invention has been identified as clone "nn229_1".
15 nn229_1 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. nn229_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred
20 to herein as "nn229_1 protein").

The nucleotide sequence of nn229_1 as presently determined is reported in SEQ ID NO:63, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the nn229_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:64. Amino
25 acids 59 to 71 of SEQ ID NO:64 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 72. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the nn229_1 protein.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone nn229_1 should be approximately 1050 bp.

The nucleotide sequence disclosed herein for nn229_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. nn229_1 demonstrated at least some similarity with sequences identified as H24014 (ym49f02.s1 Homo sapiens cDNA clone 51480 3'), R08508 (ye95h01.r1 Homo sapiens cDNA clone 125521 5' similar to gb|M87910|HUMALNE34 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb J02931 TISSUE FACTOR PRECURSOR (HUMAN)), and Z96508 (H.sapiens telomeric DNA sequence, clone 22QTEL030, read 22QTELOO030.seq). Based upon sequence similarity, nn229_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the nn229_1 protein sequence centered around amino acid 20 of SEQ ID NO:64. The nucleotide sequence of nn229_1 indicates that it may contain a MER20 repetitive element.

Clone "np156_1"

A polynucleotide of the present invention has been identified as clone "np156_1". np156_1 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. np156_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "np156_1 protein").

The nucleotide sequence of np156_1 as presently determined is reported in SEQ ID NO:65, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the np156_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:66. Amino acids 6 to 18 of SEQ ID NO:66 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the np156_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone np156_1 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for np156_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. np156_1 demonstrated at least some similarity with sequences

identified as AA298580 (EST114211 HSC172 cells I Homo sapiens cDNA 5' end), AA447514 (zw81a05.s1 Soares testis NHT Homo sapiens cDNA clone 782576 3'), AC002309 (** SEQUENCING IN PROGRESS ** Human Chromosome 22q11 Cosmid Clone 63e9; HTGS phase 1, 3 unordered pieces), AF007269 (Arabidopsis thaliana BAC IG002N01), and N53641 (yz04g03.r1 Homo sapiens cDNA clone 282100 5'). Based upon sequence similarity, np156_1 proteins and each similar protein or peptide may share at least some activity.

Clone "bg570_1"

10 A polynucleotide of the present invention has been identified as clone "bg570_1". bg570_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bg570_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bg570_1 protein").

The nucleotide sequence of bg570_1 as presently determined is reported in SEQ ID NO:67, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bg570_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:68. Amino acids 33 to 45 of SEQ ID NO:68 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 46. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the bg570_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bg570_1 should be approximately 900 bp.

The nucleotide sequence disclosed herein for bg570_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bg570_1 demonstrated at least some similarity with sequences identified as T03370 (IB1429 Infant brain, Bento Soares Homo sapiens cDNA clone IB1429 3'end). Based upon sequence similarity, bg570_1 proteins and each similar protein or peptide may share at least some activity.

Clone "bi120_2"

A polynucleotide of the present invention has been identified as clone "bi120_2". bi120_2 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bi120_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bi120_2 protein").

The nucleotide sequence of bi120_2 as presently determined is reported in SEQ ID
10 NO:69, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bi120_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:70. Amino acids 39 to 51 of SEQ ID NO:70 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 52. Due to the hydrophobic nature
15 of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the bi120_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bi120_2 should be approximately 1800 bp.

20 The nucleotide sequence disclosed herein for bi120_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bi120_2 demonstrated at least some similarity with sequences identified as AA232119 (zr24a12.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 664318 5' similar to WP:C11H1.2 CE05261), D20759 (Human HL60
25 3'directed MboI cDNA, HUMGS01738, clone mp1051), N28753 (yx67h11.r1 Homo sapiens cDNA clone), N28806 (yx70g12.r1 Homo sapiens cDNA clone 267142 5'), N35232 (yy21d02.s1 Homo sapiens cDNA clone 271875 3'), W73805 (zd50g02.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344114 5'), Z61133 (H.sapiens CpG island DNA genomic MseI fragment, clone 45g1, forward read cpg45g1.ft1a), and Z70205
30 (Caenorhabditis elegans cosmid C11H1, complete sequence). bi120_2 also demonstrated at least some similarity with CpG island DNA. The predicted amino acid sequence disclosed herein for bi120_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bi120_2 protein

demonstrated at least some similarity to sequences identified as Z70205 (C11H1.2 [Caenorhabditis elegans]). Based upon sequence similarity, bi120_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential transmembrane domains within the bi120_2 protein sequence, centered around amino acids 20, 80, 110, 150, and 290 of SEQ ID NO:70, respectively. There may be a frameshift in the full-clone sequence (somewhere within base pairs 990-1010 of SEQ ID NO:69). This frameshift from reading frame 3 to reading frame 1 would extend the open reading frame from 309 amino acids to at least 460 amino acids and add three more potential transmembrane domains to the protein. There also appears to be another frameshift occurring around base pair 1450 of SEQ ID NO:69 which shifts the open reading frame back into frame 3, adding approximately 20 more codons to the open reading frame sequence.

Clone "bn594_1"

A polynucleotide of the present invention has been identified as clone "bn594_1". bn594_1 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bn594_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bn594_1 protein").

The nucleotide sequence of bn594_1 as presently determined is reported in SEQ ID NO:71, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bn594_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:72.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bn594_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for bn594_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bn594_1 demonstrated at least some similarity with sequences identified as J03071 (Human growth hormone (GH-1 and GH-2) and chorionic somatomammotropin (CS-1, CS-2 and CS-5) genes, complete cds). Based upon sequence similarity, bn594_1 proteins and each similar protein or peptide may share at least some

activity. The TopPredII computer program predicts a potential transmembrane domain within the bn594_1 protein sequence centered around amino acid 52 of SEQ ID NO:72; this region is also a potential signal sequence, with the mature protein starting at amino acid 53 of SEQ ID NO:72. The nucleotide sequence of bn594_1 indicates that it may
5 contain one or more of the following types of repetitive elements: ALU, GAAA.

Clone "en554_1"

A polynucleotide of the present invention has been identified as clone "en554_1". en554_1 was isolated from a human fetal brain cDNA library using methods which are
10 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. en554_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "en554_1 protein").

15 The nucleotide sequence of en554_1 as presently determined is reported in SEQ ID NO:73, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the en554_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:74. Amino acids 15 to 27 of SEQ ID NO:74 are a predicted leader/signal sequence, with the predicted
20 mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the en554_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing
25 clone en554_1 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for en554_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. en554_1 demonstrated at least some similarity with sequences identified as AA625842 (zv87d08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
30 766767 3') and R54550 (yg75h06.r1 Homo sapiens cDNA clone 39297 5'). Based upon sequence similarity, en554_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of en554_1 indicates that it may contain repetitive elements in the region between base pairs 849 and 1023 of SEQ ID NO:73.

Clone "na474_10"

A polynucleotide of the present invention has been identified as clone "na474_10". na474_10 was isolated from a human adult brain (corpus callosum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. na474_10 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "na474_10 protein").

The nucleotide sequence of na474_10 as presently determined is reported in SEQ ID NO:75, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the na474_10 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:76. Amino acids 69 to 81 of SEQ ID NO:76 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 82. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the na474_10 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone na474_10 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for na474_10 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. na474_10 demonstrated at least some similarity with sequences identified as AA262604 (zs23f01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686041 3' similar to contains Alu repetitive element), AA450131 (zx42a02.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 789098 5'), U72661 (Human ninjurin1 mRNA, complete cds), and W38567 (zb20h04.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 302647 5'). The predicted amino acid sequence disclosed herein for na474_10 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted na474_10 protein demonstrated at least some similarity to sequences identified as U72661 (ninjurin1 [Homo sapiens]). Based upon sequence similarity, na474_10 proteins and each similar protein or peptide may share at least some activity. Ninjurin is a cell-surface protein and adhesion molecule which is induced by nerve injury and promotes axonal growth.

Ninjurin is capable of mediating homophilic adhesion and can promote neurite extension of dorsal root ganglion neurons *in vitro*. It is thought to play a role in nerve regeneration and in the formation and function of other tissues (Araki *et al.*, 1996, *Neuron* 17(2):353-361, incorporated herein by reference). na474_10 and ninjurin appear to define a novel family
5 of adhesion molecules.

na474_10 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 15 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

10 Clone "nn16_10"

A polynucleotide of the present invention has been identified as clone "nn16_10". nn16_10 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis
15 of computer analysis of the amino acid sequence of the encoded protein. nn16_10 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "nn16_10 protein").

The nucleotide sequence of nn16_10 as presently determined is reported in SEQ ID NO:77, and includes a poly(A) tail. What applicants presently believe to be the proper
20 reading frame and the predicted amino acid sequence of the nn16_10 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:78. Amino acids 14 to 26 of SEQ ID NO:78 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain
25 should the predicted leader/signal sequence not be separated from the remainder of the nn16_10 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone nn16_10 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for nn16_10 was searched against the
30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. nn16_10 demonstrated at least some similarity with sequences identified as R46973 (Y224 *Rattus norvegicus* cDNA clone Y224 5' end), U43404 (*Sus scrofa* ameloblastin mRNA, complete cds), W13000 (mb21d12.r1 Soares mouse

p3NMF19.5 *Mus musculus* cDNA clone 330071 5'), and W36463 (mb71c12.r1 Soares mouse p3NMF19.5 *Mus musculus* cDNA clone 334870 5'). The predicted amino acid sequence disclosed herein for nn16_10 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted
5 nn16_10 protein demonstrated at least some similarity to sequences identified as U43404 (ameloblastin [*Sus scrofa*]), and to the ameloblastin proteins of rat (and other species). Ameloblastin is a unique ameloblast-specific gene product that may be important in enamel matrix formation and mineralization (Krebsbach *et al.*, 1996, *J. Biol. Chem.* 271: 4431, incorporated herein by reference). Rat ameloblastin is 442 amino acids and is a
10 tooth-specific enamel matrix protein. Immunohistochemical data show staining of golgi and of secretory granules of the secretory ameloblast, in addition to the entire thickness of the enamel matrix. The rat ameloblastin protein is synthesized as a 55 kDa core protein which undergoes extensive post-translational modifications with O-linked oligo-
saccharides to become the 65 kDa secretory form (Uchida *et al.*, 1997, *J. Histochem. Cytochem.* 45(10):1329-1340, incorporated herein by reference). Based upon sequence
15 similarity, nn16_10 proteins and each similar protein or peptide may share at least some activity.

nn16_10 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 84 kDa was detected in conditioned medium and
20 membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "np189_9"

A polynucleotide of the present invention has been identified as clone "np189_9". np189_9 was isolated from a human fetal kidney (293 cell line) cDNA library using
25 methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. np189_9 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "np189_9 protein").

30 The nucleotide sequence of np189_9 as presently determined is reported in SEQ ID NO:79, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the np189_9 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:80. Amino

acids 41 to 53 of SEQ ID NO:80 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 54. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the
5 np189_9 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone np189_9 should be approximately 2100 bp.

The nucleotide sequence disclosed herein for np189_9 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
10 FASTA search protocols. np189_9 demonstrated at least some similarity with sequences identified as AA035196 (zk27f12.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 471791 3'), AA336568 (EST41447 Endometrial tumor Homo sapiens cDNA 5' end), AA420972 (zt86a11.s1 Soares testis NHT Homo sapiens cDNA clone 729212 3'), and H38460 (yp69h08.s1 Homo sapiens cDNA clone 192735 3'). Based upon sequence
15 similarity, np189_9 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the np189_9 protein sequence centered around amino acid 38 of SEQ ID NO:80.

20 Clone "ny226_1"

A polynucleotide of the present invention has been identified as clone "ny226_1". ny226_1 was isolated from a human adult brain (substantia nigra) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis
25 of computer analysis of the amino acid sequence of the encoded protein. ny226_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ny226_1 protein").

The nucleotide sequence of ny226_1 as presently determined is reported in SEQ ID NO:81, and includes a poly(A) tail. What applicants presently believe to be the proper
30 reading frame and the predicted amino acid sequence of the ny226_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:82.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ny226_1 should be approximately 3175 bp.

The nucleotide sequence disclosed herein for ny226_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ny226_1 demonstrated at least some similarity with sequences identified as AC002463 (Human BAC clone RG302F04 from 7q31, complete sequence),
5 R07637 (ye98e03.s1 Homo sapiens cDNA clone 125788 3'), and Z78730 (H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA15C3). Based upon sequence similarity, ny226_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the ny226_1 protein sequence centered around amino acid 22 of SEQ ID NO:82;
10 this region is also a putative signal sequence, with the mature protein starting at amino acid 23 of SEQ ID NO:82. The nucleotide sequence of ny226_1 indicates that it may contain one or more repetitive elements, including ALU repetitive elements.

Clone "pe159_1"

15 A polynucleotide of the present invention has been identified as clone "pe159_1". pe159_1 was isolated from a human adult blood (chronic myelogenous leukemia K5) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded
20 protein. pe159_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pe159_1 protein").

The nucleotide sequence of pe159_1 as presently determined is reported in SEQ ID NO:83, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pe159_1 protein
25 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:84.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pe159_1 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for pe159_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
30 FASTA search protocols. pe159_1 demonstrated at least some similarity with sequences identified as AA372974 (EST84925 Colon adenocarcinoma IV Homo sapiens cDNA 5' end), AC002377 (Human PAC clone DJ222H05), AC002519 (** SEQUENCING IN PROGRESS**) Human chromosome 16p11.2 BAC clone CIT987SK-A-355G7; HTGS phase

2, 1 ordered pieces), H45355 (yn99b01.r1 Homo sapiens cDNA clone 176521 5'), W39648 (zc19c09.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 322768 5'), and Z84816 (Human DNA sequence from PAC 2A2 on chromosome X contains ESTs). The predicted amino acid sequence disclosed herein for pe159_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pe159_1 protein demonstrated at least some similarity to sequences identified as M84237 (integrin beta-1 subunit [Homo sapiens]) and R96800 (Human histiocyte-secreted factor HSF). Based upon sequence similarity, pe159_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of pe159_1 indicates that it may contain one or more of the following types of repetitive elements: Alu, SVA, MER3.

Clone "pj314_8"

A polynucleotide of the present invention has been identified as clone "pj314_8". pj314_8 was isolated from a human fetal carcinoma (cell type NTD2 treated with retinoic acid for 23 days) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pj314_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pj314_8 protein").

The nucleotide sequence of pj314_8 as presently determined is reported in SEQ ID NO:85, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pj314_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:86. Amino acids 23 to 35 of SEQ ID NO:86 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 36. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pj314_8 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pj314_8 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for pj314_8 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. pj314_8 demonstrated at least some similarity with sequences identified as H98510 (yv90g02.r1 Homo sapiens cDNA clone), U03019 (Human melanoma growth stimulatory activity beta (MGSA beta) gene, partial cds), U25660 (Dictyostelium discoideum actin gene, partial cds), W67504 (zd40f09.s1 Soares fetal heart NbHH19W
5 Homo sapiens cDNA clone 343145 3'), Z99358 (Homo sapiens mRNA; expressed sequence tag; clone DKFZphamy1_1a3, 5' read), and Z99359 (Homo sapiens mRNA; expressed sequence tag; clone DKFZphamy1_1a3, 3' read). The predicted amino acid sequence disclosed herein for pj314_8 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pj314_8 protein
10 demonstrated at least some similarity to sequences identified as U16359 (nitric oxide synthase [Rattus norvegicus]). Based upon sequence similarity, pj314_8 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of pj314_8 indicates that it may contain one or more of the following types of repetitive elements: AC repeats, PAB repeats, CA repeats.

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Clone "bp870_1"

A polynucleotide of the present invention has been identified as clone "bp870_1". bp870_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
20 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bp870_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bp870_1 protein").

The nucleotide sequence of bp870_1 as presently determined is reported in SEQ
25 ID NO:87, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bp870_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:88. Amino acids 9 to 21 of SEQ ID NO:88 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature
30 of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the bp870_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bp870_1 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for bp870_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bp870_1 demonstrated at least some similarity with sequences identified as AA229935 (nc51g10.r1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1011714 similar to contains Alu repetitive element;contains element MER4 repetitive element), H12643 (yj13a04.r1 Homo sapiens cDNA clone 148590 5'), and H12594 (yj13a04.s1 Homo sapiens cDNA clone 148590 3' similar to contains Alu repetitive element). Based upon sequence similarity, bp870_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of bp870_1 indicates that it may contain a simple repeat region and at least one copy of an Alu repetitive element.

bp870_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 23 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "bx141_2"

A polynucleotide of the present invention has been identified as clone "bx141_2". bx141_2 was isolated from a human adult ovary (PA-1 teratocarcinoma, pool of retinoic-acid-treated, activin-treated, and untreated tissue) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bx141_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bx141_2 protein").

The nucleotide sequence of bx141_2 as presently determined is reported in SEQ ID NO:89, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bx141_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:90. Amino acids 30 to 42 of SEQ ID NO:90 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 43. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain

should the predicted leader/signal sequence not be separated from the remainder of the bx141_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bx141_2 should be approximately 1800 bp.

- 5 The nucleotide sequence disclosed herein for bx141_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bx141_2 demonstrated at least some similarity with sequences identified as AA173353 (zp32b01.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 611113 5' similar to SW:A15_HUMAN P41732 CELL SURFACE
- 10 GLYCOPROTEIN A15), AA375927 (EST88303 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to cell surface glycoprotein), D10653 (Human mRNA for cell surface glycoprotein, complete cds), H64050 (yr58c07.r1 Homo sapiens cDNA clone 209484 5' similar to SP:S39262 S39262 PLATELET CELL SURFACE GLYCOPROTEIN), and R41866 (yg12f04.s1 Homo sapiens cDNA clone 31854 3'). The predicted amino acid sequence
- 15 disclosed herein for bx141_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bx141_2 protein demonstrated at least some similarity to sequences identified as D10653 (HUMA15_1 cell surface glycoprotein [Homo sapiens]) and D29808 (HUMTALLA1_1 TALLA-1 [Homo sapiens]). The human cell surface glycoprotein ("D10653 protein") is a protein of 244
- 20 amino acids which contains four potential transmembrane domains and four possible N-linked glycosylation sites. A computer-aided comparison showed a marked similarity between D10653 protein and several other membrane proteins: CD9, CD37, CD53, TAPA-1, Sm23, CO-029, and ME491/CD63; also, D10653 protein is similar to the ME491/CD63 protein superfamily. bx141_2 protein also shows some similarity to the
- 25 human and mouse ME491 and CD63 proteins. Based upon sequence similarity, bx141_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four potential transmembrane domains within the bx141_2 protein sequence centered around amino acids 31, 70, 104, and 222 of SEQ ID NO:90, respectively.
- 30 bx141_2 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 24 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "cw272_7"

A polynucleotide of the present invention has been identified as clone "cw272_7". cw272_7 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cw272_7 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw272_7 protein").

The nucleotide sequence of cw272_7 as presently determined is reported in SEQ
10 ID NO:91, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cw272_7 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:92. Amino acids 48 to 60 of SEQ ID NO:92 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 61. Due to the hydrophobic nature
15 of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cw272_7 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw272_7 should be approximately 2300 bp.

20 The nucleotide sequence disclosed herein for cw272_7 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. While no clear hits were found in these databases, cw272_7 protein does show some similarity to bone morphogenetic proteins and procollagens.

25 Clone "nh328_5"

A polynucleotide of the present invention has been identified as clone "nh328_5". nh328_5 was isolated from a human adult brain (thalamus) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of
30 computer analysis of the amino acid sequence of the encoded protein. nh328_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "nh328_5 protein").

The nucleotide sequence of nh328_5 as presently determined is reported in SEQ ID NO:93, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the nh328_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:94. Amino acids 60 to 72 of SEQ ID NO:94 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 73. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the nh328_5 protein.

- 10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone nh328_5 should be approximately 2200 bp.

- The nucleotide sequence disclosed herein for nh328_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. nh328_5 demonstrated at least some similarity with sequences identified as AA426157 (zv83a09.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 760216 5'), D17160 (Human HepG2 3' region MboI cDNA, clone hmd2d01m3), D56329 (Human fetal brain cDNA 5'-end GEN-424F08), N62903 (yy67e09.s1 Homo sapiens cDNA clone 278632 3'), R88485 (ym94e01.r1 Homo sapiens cDNA clone 166584 5'), and T26592 (AB329E6R Homo sapiens cDNA clone LLAB329E6 5'). Based upon sequence similarity, nh328_5 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of nh328_5 indicates that it may contain some GAA/TIGGER repeat sequences.

- nh328_5 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 70 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "nm214_3"

- A polynucleotide of the present invention has been identified as clone "nm214_3". nm214_3 was isolated from a human adult blood (erythroleukemia TF-1) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. nm214_3

is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "nm214_3 protein").

The nucleotide sequence of nm214_3 as presently determined is reported in SEQ ID NO:95, and includes a poly(A) tail. What applicants presently believe to be the proper
5 reading frame and the predicted amino acid sequence of the nm214_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:96.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone nm214_3 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for nm214_3 was searched against the
10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. nm214_3 demonstrated at least some similarity with sequences identified as D10083 (Human RGH1 gene), D11078 (Human RGH2 gene), R68638 (y106g11.s1 Homo sapiens cDNA clone 1385003'), U88895 (Human endogenous retrovirus H D1 leader region/integrase-derived ORF1, ORF2, and putative envelope protein
15 mRNA, complete cds), Z95327 (Human DNA sequence ***SEQUENCING IN PROGRESS *** from clone 347M6; HTGS phase 1), and Z97183 (Human DNA sequence ***SEQUENCING IN PROGRESS *** from clone ICB2046; HTGS phase 1). The predicted amino acid sequence disclosed herein for nm214_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The
20 predicted nm214_3 protein demonstrated at least some similarity to sequences identified as U88895 (HERV-H integrase/envelope region [Homo sapiens]). Based upon sequence similarity, nm214_3 proteins and each similar protein or peptide may share at least some activity. The nm214_3 protein has a putative signal sequence at amino acids 13 to 25 of SEQ ID NO:96, with the mature protein starting at amino acid 26. The TopPredII
25 computer program predicts a potential transmembrane domain within the nm214_3 protein sequence centered around amino acid 90 of SEQ ID NO:96.

nm214_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 13 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

30

Clone "nn320_2"

A polynucleotide of the present invention has been identified as clone "nn320_2". nn320_2 was isolated from a human fetal kidney (293 cell line) cDNA library using

methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. nn320_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred
5 to herein as "nn320_2 protein").

The nucleotide sequence of nn320_2 as presently determined is reported in SEQ ID NO:97, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the nn320_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:98. Amino
10 acids 4 to 16 of SEQ ID NO:98 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the nn320_2 protein.

15 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone nn320_2 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for nn320_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. nn320_2 demonstrated at least some similarity with sequences
20 identified as AA423969 (zv79h04.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 759895 5') and AA423988 (zv79h04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 759895 3'). The predicted amino acid sequence disclosed herein for nn320_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted nn320_2 protein demonstrated at least some
25 similarity to sequences identified as M60351 (filamentous hemagglutinin [Bordetella pertussis]) and R05041 (Filamentous haemagglutinin A). The predicted nn320_2 protein also demonstrated similarity to a variety of proteases and enzyme precursors such as trypsinogen precursor. Based upon sequence similarity, nn320_2 proteins and each similar protein or peptide may share at least some activity.

30 nn320_2 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 58 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "pp392_3"

A polynucleotide of the present invention has been identified as clone "pp392_3". pp392_3 was isolated from a human adult blood (lymphoblastic leukemia MOLT-4) cDNA library using methods which are selective for cDNAs encoding secreted proteins
5 (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pp392_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pp392_3 protein").

The nucleotide sequence of pp392_3 as presently determined is reported in SEQ
10 ID NO:99, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pp392_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:100.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pp392_3 should be approximately 2100 bp.

15 The nucleotide sequence disclosed herein for pp392_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pp392_3 demonstrated at least some similarity with sequences identified as AA117686 (mo64c07.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone 558348 5') and AL008726 (Human DNA sequence *** SEQUENCING IN
20 PROGRESS *** from clone 337O18; HTGS phase 1). Based upon sequence similarity, pp392_3 proteins and each similar protein or peptide may share at least some activity. The pp392_3 protein has a putative signal sequence at amino acids 196 to 208 of SEQ ID NO:100, with the mature protein starting at amino acid 209. The TopPredII computer program predicts three potential transmembrane domains within the pp392_3 protein
25 sequence centered around amino acids 20, 130, and 310 of SEQ ID NO:100, respectively.

The nucleotide sequence of pp392_3 indicates that it may contain a CA repetitive element.

pp392_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 56 kDa was detected in membrane fractions using SDS
30 polyacrylamide gel electrophoresis.

Clone "ya13_1"

A polynucleotide of the present invention has been identified as clone "ya13_1". ya13_1 was isolated from a human adult testes cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ya13_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ya13_1 protein").

The nucleotide sequence of ya13_1 as presently determined is reported in SEQ ID NO:101, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ya13_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:102. Amino acids 72 to 84 of SEQ ID NO:102 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 85. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ya13_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ya13_1 should be approximately 750 bp.

The nucleotide sequence disclosed herein for ya13_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ya13_1 demonstrated at least some similarity with sequences identified as AA190721 (zp88a07.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 627252 5'). Based upon sequence similarity, ya13_1 proteins and each similar protein or peptide may share at least some activity.

Clone "yb37_1"

A polynucleotide of the present invention has been identified as clone "yb37_1". yb37_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb37_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb37_1 protein").

The nucleotide sequence of yb37_1 as presently determined is reported in SEQ ID NO:103, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb37_1 protein

corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:104. Amino acids 28 to 40 of SEQ ID NO:104 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 41. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yb37_1 protein. The TopPredII computer program predicts an additional potential transmembrane domain within the yb37_1 protein sequence centered around amino acid 144 of SEQ ID NO:104.

Another possible reading frame and predicted amino acid sequence encoded by yb37_1 is reported in SEQ ID NO:275; amino acids 49 to 61 of SEQ ID NO:275 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 62. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:275.

The nucleotide sequence disclosed herein for yb37_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database. The nucleotide sequence of yb37_1 indicates that it may contain one or more A/TAAA repetitive elements.

yb37_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 33 kDa was detected in conditioned medium fractions using SDS polyacrylamide gel electrophoresis.

Clone "yb39_1"

A polynucleotide of the present invention has been identified as clone "yb39_1". yb39_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb39_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb39_1 protein").

The nucleotide sequence of yb39_1 as presently determined is reported in SEQ ID NO:105, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb39_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:106. Amino acids 21 to 33 of SEQ ID NO:106 are a predicted leader/signal sequence, with the

predicted mature amino acid sequence beginning at amino acid 34. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yb39_1 protein.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb39_1 should be approximately 825 bp.

 The nucleotide sequence disclosed herein for yb39_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

10

Clone "bd577_1"

 A polynucleotide of the present invention has been identified as clone "bd577_1". bd577_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
15 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bd577_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bd577_1 protein").

 The nucleotide sequence of bd577_1 as presently determined is reported in SEQ
20 ID NO:107, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bd577_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:108. Amino acids 42 to 54 of SEQ ID NO:108 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 55. Due to the
25 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the bd577_1 protein.

 Another possible reading frame and predicted amino acid sequence encoded by base pairs 23 to 412 of bd577_1 SEQ ID NO:107 is reported in SEQ ID NO:276; the amino
30 acid sequence of SEQ ID NO:276 has a possible signal sequence from amino acids 57 to 69, with the predicted mature amino acid sequence beginning at amino acid 70. The open reading frames corresponding to SEQ ID NO:276 and SEQ ID NO:108 could be joined if a frameshift were introduced into the nucleotide sequence of SEQ ID NO:107.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bd577_1 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for bd577_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bd577_1 demonstrated at least some similarity with sequences identified as AA306618 (EST177563 Jurkat T-cells VI Homo sapiens cDNA 5' end) and R20055 (yg39b06.r1 Homo sapiens cDNA clone 34805 5'). Based upon sequence similarity, bd577_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the bd577_1 protein sequence centered around amino acids 42 and 230 of SEQ ID NO:108.

bd577_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 56 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

15 Clone "bv280_3"

A polynucleotide of the present invention has been identified as clone "bv280_3". bv280_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bv280_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bv280_3 protein").

The nucleotide sequence of bv280_3 as presently determined is reported in SEQ ID NO:109, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bv280_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:110. Amino acids 10 to 22 of SEQ ID NO:110 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the bv280_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bv280_3 should be approximately 1900 bp.

The nucleotide sequence disclosed herein for bv280_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bv280_3 demonstrated at least some similarity with sequences identified as AA095665 (l5468.seq.F Fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'), AA577430 (nm96g10.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076130 similar to TR:G945383 G945383 CARBOXYPEPTIDASE), F06654 (H. sapiens partial cDNA sequence; clone c-1ga12), F08501 (H. sapiens partial cDNA), and H10119 (ym03f03.r1 Homo sapiens cDNA clone 46734 5' similar to SP:A41612 A41612 VITELLOGENIC CARBOXYPEPTIDASE). The predicted amino acid sequence disclosed herein for bv280_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bv280_3 protein demonstrated at least some similarity to sequences identified as L46594 (carboxypeptidase [Aedes aegypti]) and R96737 (A. niger Bo-1 carboxypeptidase Y). Based upon sequence similarity, bv280_3 proteins and each similar protein or peptide may share at least some activity. The bv280_3 protein also has a serine carboxipeptidase active site motif (residues 195-212). This motif is highly specific to serine carboxypeptidases and is not found in any other type of protein in the Swiss-Prot database. The bv280_3 protein also has one copy of the crystallins beta and gamma 'Greek key' motif signature. The TopPredII computer program predicts another potential transmembrane domain within the bv280_3 protein sequence centered around amino acid 110 of SEQ ID NO:110.

bv280_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 61 kDa was detected in conditioned medium fractions using SDS polyacrylamide gel electrophoresis.

25 Clone "co315_3"

A polynucleotide of the present invention has been identified as clone "co315_3". co315_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. co315_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "co315_3 protein").

The nucleotide sequence of co315_3 as presently determined is reported in SEQ ID NO:111, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the co315_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:112.

5 Amino acids 51 to 63 of SEQ ID NO:112 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 64. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the co315_3 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone co315_3 should be approximately 710 bp.

The nucleotide sequence disclosed herein for co315_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. co315_3 demonstrated at least some similarity with sequences
15 identified as AA031371 (zk15e11.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 470636 3'), AA026051 (ze86a07.s1 Soares fetal heart NbHH19W Homo sapiens), AA393961 (zt78b10.r1 Soares testis NHT Homo sapiens cDNA clone 728443 5'), AA481047 (aa29c06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814666 3'), H46323 (yo15c05.r1 Homo sapiens cDNA clone 177992 5'), N23329 (yx78h09.s1 Homo sapiens
20 cDNA clone 267905 3'), and R43942 (yg22f02.s1 Homo sapiens cDNA clone 33080 3' similar to gb:M14648 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (HUMAN)). Based upon sequence similarity, co315_3 proteins and each similar protein or peptide may share at least some activity.

25 Clone "ij226_6"

A polynucleotide of the present invention has been identified as clone "ij226_6". ij226_6 was isolated from a human adult blood (peripheral blood mononuclear cells treated with granulocyte-colony stimulating factor *in vivo*) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637),
30 or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ij226_6 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ij226_6 protein").

The nucleotide sequence of ij226_6 as presently determined is reported in SEQ ID NO:113, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ij226_6 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:114.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ij226_6 should be approximately 2300 bp.

 The nucleotide sequence disclosed herein for ij226_6 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ij226_6 demonstrated at least some similarity with sequences
10 identified as AE000658 (Homo sapiens T-cell receptor alpha delta locus from bases 1 to 250529 (section 1 of 5) of the Complete Nucleotide Sequence), AF004231 (Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds), G35352 (STS h14a108 5), H54023 (yq88h01.s1 Homo sapiens cDNA), H54181 (yq88h01.r1 Homo sapiens cDNA clone 202897 5'), T18551 (Human polycystic kidney disease normal
15 PKD1 gene), and Z82206 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 370M22; HTGS phase 1). The predicted amino acid sequence disclosed herein for ij226_6 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ij226_6 protein demonstrated at least some similarity to sequences identified as M22334 (unknown protein [Homo
20 sapiens]). Based upon sequence similarity, ij226_6 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the ij226_6 protein sequence centered around amino acids 37 and 62 of SEQ ID NO:114. The nucleotide sequence of ij226_6 indicates that it may contain one or more of the following repetitive elements: L1, Alu, SVA.

25

Clone "nf443_1"

 A polynucleotide of the present invention has been identified as clone "nf443_1". nf443_1 was isolated from a human adult brain (substantia nigra) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No.
30 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. nf443_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "nf443_1 protein").

The nucleotide sequence of nf443_1 as presently determined is reported in SEQ ID NO:115, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the nf443_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:116.

5 Amino acids 21 to 43 of SEQ ID NO:116 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 44. Due to the hydrophobic nature of this possible leader/signal sequence, it is likely to act as a transmembrane domain should the leader/signal sequence not be separated from the remainder of the nf443_1 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone nf443_1 should be approximately 3800 bp.

The nucleotide sequence disclosed herein for nf443_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. nf443_1 demonstrated at least some similarity with sequences
15 identified as AA417092 (zu07a12.s1 Soares testis NHT Homo sapiens cDNA clone 731134 3'), AA421511 (zu07a12.r1 Soares testis NHT Homo sapiens cDNA clone 731134 5'), T23707 (Human gene signature HUMGS05583), and U61233 (Bos taurus tubulin-folding cofactor D mRNA, complete cds). The predicted amino acid sequence disclosed herein for nf443_1 was searched against the GenPept and GeneSeq amino acid sequence
20 databases using the BLASTX search protocol. The predicted nf443_1 protein demonstrated at least some similarity to sequences identified as U61233 (cofactor D [Bos taurus]). Based upon sequence similarity, nf443_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of nf443_1 indicates that it may contain an Alu repetitive element.

25 nf443_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 10 kDa was detected in conditioned medium fractions using SDS polyacrylamide gel electrophoresis.

Clone "nt429_1"

30 A polynucleotide of the present invention has been identified as clone "nt429_1". nt429_1 was isolated from a human adult brain (corpus callosum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis

of computer analysis of the amino acid sequence of the encoded protein. nt429_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "nt429_1 protein").

5 The nucleotide sequence of nt429_1 as presently determined is reported in SEQ ID NO:117, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the nt429_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:118. Another possible reading frame and predicted amino acid sequence, encoded by base pairs 399 to 731 of nt429_1 SEQ ID NO:117, is reported in SEQ ID NO:277; the amino acid
10 sequence of SEQ ID NO:277 is hydrophobic in nature near its carboxyl terminus. The overlapping open reading frames corresponding to SEQ ID NO:118 and SEQ ID NO:277 could be joined if a frameshift were introduced into the nucleotide sequence of SEQ ID NO:117.

The EcoRI/NotI restriction fragment obtainable from the deposit containing
15 clone nt429_1 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for nt429_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the database. The nucleotide
20 sequence of nt429_1 indicates that it may contain one or more of the following repetitive elements: Alu, SVA, A.

Clone "pe503_1"

A polynucleotide of the present invention has been identified as clone "pe503_1". pe503_1 was isolated from a human adult blood (chronic myelogenous leukemia K5)
25 cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pe503_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pe503_1 protein").

30 The nucleotide sequence of pe503_1 as presently determined is reported in SEQ ID NO:119, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pe503_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:120.

Amino acids 79 to 91 of SEQ ID NO:120 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 92. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pe503_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pe503_1 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for pe503_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pe503_1 demonstrated at least some similarity with sequences identified as AA298572 (EST114204 HSC172 cells I Homo sapiens cDNA 5' end), AA595242 (no33a12.s1 NCI_CGAP_Pr23 Homo sapiens cDNA clone IMAGE:1102462), H60941 (yr14g06.r1 Homo sapiens cDNA clone 205306 5'), H75686 (yr77g08.r1 Homo sapiens cDNA clone 211358 5'), and R61206 (yh06d11.r1 Homo sapiens cDNA clone 42649 5'). Based upon sequence similarity, pe503_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four potential transmembrane domains within the pe503_1 protein sequence centered around amino acids 50, 84, 107, and 148 of SEQ ID NO:120, respectively.

pe503_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 19 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "pe834_6"

A polynucleotide of the present invention has been identified as clone "pe834_6". pe834_6 was isolated from a human adult blood (chronic myelogenous leukemia K5) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pe834_6 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pe834_6 protein").

The nucleotide sequence of pe834_6 as presently determined is reported in SEQ ID NO:121, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pe834_6 protein

corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:122. Another possible reading frame and predicted amino acid sequence, encoded by base pairs 414 to 725 of pe834_6 SEQ ID NO:121, is reported in SEQ ID NO:278; the amino acid sequence of SEQ ID NO:278 is hydrophobic in nature near its carboxyl terminus. The overlapping open reading frames corresponding to SEQ ID NO:122 and SEQ ID NO:278 could be joined if a frameshift were introduced into the nucleotide sequence of SEQ ID NO:121.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pe834_6 should be approximately 1300 bp.

10 The nucleotide sequence disclosed herein for pe834_6 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pe834_6 demonstrated at least some similarity with sequences identified as AA054341 (zl68f04.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 5097913'), N21462 (yx57c10.s1 Homo sapiens cDNA clone 2658423'), N34010 (yx75g07.r1
15 Homo sapiens cDNA clone 2676125'), and T90232 (ye15c09.r1 Homo sapiens cDNA clone 1178085'). Based upon sequence similarity, pe834_6 proteins and each similar protein or peptide may share at least some activity.

pe834_6 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 17 kDa was detected in membrane fractions using SDS
20 polyacrylamide gel electrophoresis.

Clone "ya10_1"

A polynucleotide of the present invention has been identified as clone "ya10_1". ya10_1 was isolated from a human adult testes cDNA library and was identified as
25 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ya10_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ya10_1 protein").

The nucleotide sequence of ya10_1 as presently determined is reported in SEQ ID NO:123, and includes a poly(A) tail. What applicants presently believe to be the proper
30 reading frame and the predicted amino acid sequence of the ya10_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:124. Amino acids 6 to 18 of SEQ ID NO:124 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the

hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ya10_1 protein.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ya10_1 should be approximately 800 bp.

The nucleotide sequence disclosed herein for ya10_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No clearly significant hits were found in these databases. BLASTX analysis of the ya10_1 protein sequence revealed some amino acid sequence
10 similarity to cystatins (cysteine protease inhibitors) of various species. Based upon this sequence similarity, ya10_1 proteins and each similar protein or peptide may share at least some activity.

Clone "yb40_1"

15 A polynucleotide of the present invention has been identified as clone "yb40_1". yb40_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb40_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb40_1 protein").

20 The nucleotide sequence of yb40_1 as presently determined is reported in SEQ ID NO:125, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb40_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:126. Amino acids 29 to 41 of SEQ ID NO:126 are a possible leader/signal sequence, with the
25 predicted mature amino acid sequence beginning at amino acid 42. Due to the hydrophobic nature of this possible leader/signal sequence, it could act as a transmembrane domain should it not be separated from the remainder of the yb40_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing
30 clone yb40_1 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for yb40_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb40_1 demonstrated at least some similarity with sequences

identified as AA595189 (no32f03.s1 NCI_CGAP_Pr23 Homo sapiens cDNA clone IMAGE:1102397), R74575 (yi58d04.r1 Homo sapiens cDNA clone 143431 5'), and T25773 (Human gene signature HUMGS08001). Based upon sequence similarity, yb40_1 proteins and each similar protein or peptide may share at least some activity.

5

Clone "cs756_2"

A polynucleotide of the present invention has been identified as clone "cs756_2". cs756_2 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
10 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cs756_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cs756_2 protein").

The nucleotide sequence of cs756_2 as presently determined is reported in SEQ ID
15 NO:127, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cs756_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:128. Amino acids 211 to 223 of SEQ ID NO:128 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 224. Due to the
20 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cs756_2 protein. The TopPredII computer program predicts a potential transmembrane domain within the cs756_2 protein sequence of SEQ ID NO:128, centered around amino acid 15 of SEQ ID NO:128; amino acids 2 to 14 of SEQ ID NO:128
25 are also a possible leader/signal sequence, with the predicted mature amino acid sequence in that case beginning at amino acid 15.

Another possible cs756_2 reading frame and predicted amino acid sequence, encoded by base pairs 385 to 825 of SEQ ID NO:127, is reported in SEQ ID NO:279; the TopPredII computer program predicts a potential transmembrane domain centered
30 around amino acid 100 of SEQ ID NO:279. The open reading frames corresponding to SEQ ID NO:279 and SEQ ID NO:128 could be joined if a frameshift were introduced into the nucleotide sequence of SEQ ID NO:127.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cs756_2 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for cs756_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cs756_2 demonstrated at least some similarity with sequences identified as AA398077 (zt58c03.s1 Soares testis NHT Homo sapiens cDNA clone 726532 3'), AA541286 (nf97e03.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:927868), W28620 (49c2 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA), and W47601 (zc35g08.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324350 5'). The predicted amino acid sequence disclosed herein for SEQ ID NO:279 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted SEQ ID NO:279 protein demonstrated at least some similarity to sequences identified as L76938 (Werner syndrome gene, complete cds [Homo sapiens]). "Werner's syndrome (WS) is an inherited disease with clinical symptoms resembling premature aging ... [the] predicted protein is 1432 amino acids in length and shows significant similarity to DNA helicases" (Yu *et al.*, 1996, *Science* 272(5259):258-262, which is incorporated by reference herein). Based upon sequence similarity, cs756_2 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of cs756_2 indicates that it may contain one or more of the following repetitive elements: MIR, MER.

Clone "ew150_1"

A polynucleotide of the present invention has been identified as clone "ew150_1". ew150_1 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ew150_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ew150_1 protein").

The nucleotide sequence of ew150_1 as presently determined is reported in SEQ ID NO:129, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ew150_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:130.

Amino acids 26 to 38 of SEQ ID NO:130 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 39. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated
5 from the remainder of the ew150_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ew150_1 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for ew150_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
10 FASTA search protocols. ew150_1 demonstrated at least some similarity with sequences identified as AA563938 (nk23b12.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE 1014335), D63209 (Human placenta cDNA 5'-end GEN-506F01), M90423 (Bacteriophage US3 lytic-enzyme), W23461 (zb33c01.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 305376 5'), and Z56916 (H.sapiens CpG DNA, clone 153b7,
15 forward read cpg153b7.ft1a). In the region around position 1514 of SEQ ID NO:129, ew150_1 also demonstrated at least some similarity with sequences encoding a mitochondrial energy-transfer proteins signature motif which is found in mitochondrial and other membrane proteins. Based upon sequence similarity, ew150_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer
20 program predicts ten potential transmembrane domains within the ew150_1 protein sequence, which are centered around amino acids 70, 106, 133, 200, 314, 349, 387, 457, 504, and 527 of SEQ ID NO:130, respectively.

Clone "gg894_13"

25 A polynucleotide of the present invention has been identified as clone "gg894_13". gg894_13 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. gg894_13 is a full-length
30 clone, including the entire coding sequence of a secreted protein (also referred to herein as "gg894_13 protein").

The nucleotide sequence of gg894_13 as presently determined is reported in SEQ ID NO:131, and includes a poly(A) tail. What applicants presently believe to be the

proper reading frame and the predicted amino acid sequence of the gg894_13 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:132. Amino acids 41 to 53 of SEQ ID NO:132 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 54. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the gg894_13 protein. Another possible gg894_13 reading frame and predicted amino acid sequence, encoded by base pairs 602 to 1129 of SEQ ID NO:131, is reported in SEQ ID NO:280. The open reading frames corresponding to SEQ ID NO:280 and SEQ ID NO:132 could be joined if a frameshift were introduced into the nucleotide sequence of SEQ ID NO:131.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone gg894_13 should be approximately 2400 bp.

The nucleotide sequence disclosed herein for gg894_13 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. gg894_13 demonstrated at least some similarity with sequences identified as H57424 (yr13a10.s1 Homo sapiens cDNA clone 205146 3'), T23885 (Human gene signature HUMGS05820), and W80358 (zh49a07.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 415380 3'). Based upon sequence similarity, gg894_13 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the gg894_13 protein sequence centered around amino acid 115 of SEQ ID NO:132. The nucleotide sequence of gg894_13 indicates that it may contain a RBMI repetitive element.

Clone "it217_2"

A polynucleotide of the present invention has been identified as clone "it217_2". it217_2 was isolated from a human adult brain (thalamus) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. it217_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "it217_2 protein").

The nucleotide sequence of it217_2 as presently determined is reported in SEQ ID NO:133, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the it217_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:134.

5 Another possible it217_2 reading frame and predicted amino acid sequence, encoded by base pairs 45 to 311 of SEQ ID NO:133, is reported in SEQ ID NO:281. Amino acids 36 to 48 of SEQ ID NO:281 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 49. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should

10 the predicted leader/signal sequence not be separated from the remainder of the it217_2 protein. The open reading frames corresponding to SEQ ID NO:281 and SEQ ID NO:134 could be joined if at least one frameshift were introduced into the nucleotide sequence of SEQ ID NO:133.

The EcoRI/NotI restriction fragment obtainable from the deposit containing

15 clone it217_2 should be approximately 2250 bp.

The nucleotide sequence disclosed herein for it217_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. it217_2 demonstrated at least some similarity with sequences identified as AA242969 (zr65h09.r1 Soares NhHMPu S1 Homo sapiens cDNA clone

20 668321 5' similar to SW SCC2_HUMAN P48594 SQUAMOUS CELL CARCINOMA ANTIGEN 2 ;contains Alu repetitive element), B44876 (HS-1060-A1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapien genomic clone Plate CT 782 Col 11 Row M), H82168 (yv78d08.r1 Homo sapiens cDNA clone), S66896 (squamous cell carcinoma antigen), U19556 (Human squamous cell carcinoma antigen 1 (SCCA1) mRNA, complete

25 cds), U19557 (Human squamous cell carcinoma antigen 2 (SCCA2) mRNA, complete cds), and U35459 (Human bomapin mRNA, complete cds). The predicted amino acid sequence disclosed herein for it217_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted it217_2 protein demonstrated at least some similarity to sequences identified as L40377 (cytoplasmic

30 antiproteinase 2 [Homo sapiens]), M34352 (ovalbumin [Gallus gallus]), M91161 (serpin [Equus caballus]), R25276 (SCC antigen), R48379 (Human megakaryocyte differentiation factor), S66896 (squamous cell carcinoma antigen, SCC antigen serine protease inhibitor [human, Peptide, 390 aa] [Homo sapiens]), U19568 (squamous cell carcinoma antigen

[Homo sapiens]), and U19576 (squamous cell carcinoma antigen [Homo sapiens]). Human bomapin may play a role in the regulation of protease activities during hematopoiesis (Riewald *et al.*, 1995, *J. Biol. Chem.* 270: 26754, which is incorporated by reference herein). Serpins are SERine Proteinase INhibitors and are considered
5 extracellular in localization. Human squamous cell carcinoma antigen (SSCA) is a member of the serpin family of proteinase inhibitors, purified from sera of cancer patients. Based upon sequence similarity, it217_2 proteins and each similar protein or peptide may share at least some activity.

10 Clone "ml235_2"

A polynucleotide of the present invention has been identified as clone "ml235_2". ml235_2 was isolated from a human adult brain (caudate nucleus) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis
15 of computer analysis of the amino acid sequence of the encoded protein. ml235_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ml235_2 protein").

The nucleotide sequence of ml235_2 as presently determined is reported in SEQ ID NO:135, and includes a poly(A) tail. What applicants presently believe to be the
20 proper reading frame and the predicted amino acid sequence of the ml235_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:136. Amino acids 3 to 15 of SEQ ID NO:136 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
25 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ml235_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ml235_2 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for ml235_2 was searched against the
30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ml235_2 demonstrated at least some similarity with sequences identified as AA160887 (zo79b05.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 593073 3'), R14349 (yf79f12.r1 Homo sapiens cDNA clone 28451 5'), and R54256

(yg74f07.r1 Homo sapiens cDNA clone 39059 5'). Based upon sequence similarity, ml235_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the ml235_2 protein sequence centered around amino acid 25 of SEQ ID NO:136.

5

Clone "mt24_2"

A polynucleotide of the present invention has been identified as clone "mt24_2". mt24_2 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
10 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. mt24_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "mt24_2 protein").

The nucleotide sequence of mt24_2 as presently determined is reported in SEQ ID
15 NO:137, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the mt24_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:138. Amino acids 30 to 42 of SEQ ID NO:138 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 43. Due to the
20 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the mt24_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone mt24_2 should be approximately 1400 bp.

25 The nucleotide sequence disclosed herein for mt24_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. mt24_2 demonstrated at least some similarity with sequences identified as AA062589 (zf68f04.r1 Soares pineal gland N3HPG Homo sapiens cDNA clone 382111 5') and T19332 (b08016t Testis 1 Homo sapiens cDNA clone b08016 5' end).
30 Based upon sequence similarity, mt24_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four potential transmembrane domains within the mt24_2 protein sequence centered around amino acids 38, 153, 167, and 232 of SEQ ID NO:138, respectively.

Clone "pe584_2"

A polynucleotide of the present invention has been identified as clone "pe584_2". pe584_2 was isolated from a human adult blood (chronic myelogenous leukemia K5) cDNA library using methods which are selective for cDNAs encoding secreted proteins
5 (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pe584_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pe584_2 protein").

The nucleotide sequence of pe584_2 as presently determined is reported in SEQ
10 ID NO:139, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pe584_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:140. Amino acids 27 to 39 of SEQ ID NO:140 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 40. Due to the
15 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pe584_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pe584_2 should be approximately 3000 bp.

20 The nucleotide sequence disclosed herein for pe584_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pe584_2 demonstrated at least some similarity with sequences identified as AA303149 (EST13039 Uterus tumor I), AA405004 (zt06e03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 712348 3'), AA481230 (aa34g01.r1
25 NCI_CGAP_GCB1 Homo sapiens cDNA clone 815184 5' similar to SW TCR2_ECOLI P02981 TETRACYCLINE RESISTANCE PROTEIN), D88315 (Mouse mRNA for tetracycline transporter-like protein, complete cds), and T10077 (seq1295 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-Ft109 5'). The predicted amino acid sequence disclosed herein for pe584_2 was searched against the GenPept and GeneSeq amino acid
30 sequence databases using the BLASTX search protocol. The predicted pe584_2 protein demonstrated at least some similarity to sequences identified as D88315 (tetracycline transporter-like protein [Mus musculus]). Mouse tetracycline transporter-like protein is a sugar transporter (Matsuo *et al.*, 1997, *Biochem. Biophys. Res. Comm.* 238: 126-192, which

is incorporated by reference herein). Based upon sequence similarity, pe584_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts eleven potential transmembrane domains within the pe584_2 protein sequence, which are centered around amino acids 32, 55, 78, 114, 142, 196, 235,
5 264, 287, 332, and 375 of SEQ ID NO:140, respectively.

Clone "pj323_2"

A polynucleotide of the present invention has been identified as clone "pj323_2". pj323_2 was isolated from a human fetal carcinoma (NTD2 cells treated with retinoic acid
10 for 23 days) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pj323_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pj323_2 protein").

15 The nucleotide sequence of pj323_2 as presently determined is reported in SEQ ID NO:141, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pj323_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:142. Amino acids 150 to 162 of SEQ ID NO:142 are a predicted leader/signal sequence, with
20 the predicted mature amino acid sequence beginning at amino acid 163. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pj323_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing
25 clone pj323_2 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for pj323_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pj323_2 demonstrated at least some similarity with sequences identified as AA160454 (zo74g05.r1 Stratagene pancreas (#937208) Homo sapiens cDNA
30 clone 592664 5'), AA398257 (zt60a08.s1 Soares testis NHT Homo sapiens cDNA clone 726710 3'), and T47284 (yb64g11.s1 Homo sapiens cDNA clone 76004 3'). The predicted amino acid sequence disclosed herein for pj323_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The

predicted pj323_2 protein demonstrated at least some similarity to human integral nuclear envelope protein, lamin B receptors from several species, and sterol reductases from several species. Lamin B receptors have hydrophobic carboxy terminal portions and hydrophilic amino terminal portions. Antibodies to lamin B receptors have been found
5 in patients with primary biliary cirrhosis. Sterol reductases demonstrate sequence similarity to the hydrophobic portions of lamin B receptors. Based upon sequence similarity, pj323_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts six potential transmembrane domains within the pj323_2 protein sequence, which are centered around amino acids 47,
10 106, 164, 187, 341, and 432 of SEQ ID NO:142, respectively.

pj323_2 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 46 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

15 Clone "yb24_1"

A polynucleotide of the present invention has been identified as clone "yb24_1". yb24_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb24_1 is a full-length clone, including the
20 entire coding sequence of a secreted protein (also referred to herein as "yb24_1 protein").

The nucleotide sequence of yb24_1 as presently determined is reported in SEQ ID NO:143, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb24_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:144.
25 Amino acids 25 to 37 of SEQ ID NO:144 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 38. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yb24_1 protein.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb24_1 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for yb24_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. yb24_1 demonstrated at least some similarity with sequences identified as AA149807 (zl47c09.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505072 3') and AB003515 (Rat mRNA for GEF-2, complete cds). Based upon sequence similarity, yb24_1 proteins and each similar protein or peptide may share at least some activity.

Clone "yb44_1"

A polynucleotide of the present invention has been identified as clone "yb44_1". yb44_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yb44_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yb44_1 protein").

The nucleotide sequence of yb44_1 as presently determined is reported in SEQ ID NO:145, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yb44_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:146. Amino acids 10 to 22 of SEQ ID NO:146 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yb44_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yb44_1 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for yb44_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yb44_1 demonstrated at least some similarity with sequences identified as AC000016 (** SEQUENCING IN PROGRESS ** EPM1/APECED region of chromosome 21, BAC clone B4P3; HTGS phase 1, 10 unordered pieces). The predicted amino acid sequence disclosed herein for yb44_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yb44_1 protein demonstrated at least some similarity to sequences identified as R72377 (Human auxillary cytochrome P450 species 2D6 variant 2 protein) and U44753 (cytochrome P450 [Drosophila melanogaster]). Based upon sequence similarity, yb44_1

proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the yb44_1 protein sequence, which are centered around amino acids 82, 128, and 361 of SEQ ID NO:146, respectively. The nucleotide sequence of yb44_1 indicates that it
5 may contain one or more of the following repetitive elements: Alu, AT, TATACA, MER44A, TACA.

Clone "bn69_15"

A polynucleotide of the present invention has been identified as clone "bn69_15".
10 bn69_15 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bn69_15 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein
15 as "bn69_15 protein").

The nucleotide sequence of bn69_15 as presently determined is reported in SEQ ID NO:147, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bn69_15 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:148.
20 Amino acids 47 to 59 of SEQ ID NO:148 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 60. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the bn69_15 protein. Another potential bn69_15 reading frame and
25 predicted amino acid sequence is encoded by basepairs 1008 to 1352 of SEQ ID NO:147 and is reported in SEQ ID NO:282.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bn69_15 should be approximately 2800 bp.

The nucleotide sequence disclosed herein for bn69_15 was searched against the
30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bn69_15 demonstrated at least some similarity with sequences identified as H80692 (yv01b10.r1 Homo sapiens cDNA clone 241435 5'), T64701 (yc48d02.r1 Homo sapiens cDNA clone 83907 5'), and W21368 (zb59c01.r1 Soares fetal

lung NbHL19W Homo sapiens cDNA clone 307872 5' similar to gb:M83186 CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-HEART PRECURSOR (HUMAN)). Based upon sequence similarity, bn69_15 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional
5 potential transmembrane domain within the bn69_15 protein sequence centered around amino acid 32 of SEQ ID NO:148.

Clone "cb110_1"

A polynucleotide of the present invention has been identified as clone "cb110_1".
10 cb110_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cb110_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as
15 "cb110_1 protein").

The nucleotide sequence of cb110_1 as presently determined is reported in SEQ ID NO:149, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cb110_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:150.
20 Amino acids 36 to 48 of SEQ ID NO:150 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 49. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cb110_1 protein.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cb110_1 should be approximately 900 bp.

The nucleotide sequence disclosed herein for cb110_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cb110_1 demonstrated at least some similarity with sequences
30 identified as AC001083 (Homo sapiens (subclone 2_a6 from BAC H75) DNA sequence, complete sequence), D28485 (Human MSMB gene for beta-microseminoprotein (MSP), promoter region and exon1), and Z98052 (Human DNA sequence *** SEQUENCING IN

PROGRESS *** from clone 505B13; HTGS phase 1). Based upon sequence similarity, cb110_1 proteins and each similar protein or peptide may share at least some activity.

Clone "ch4_11"

5 A polynucleotide of the present invention has been identified as clone "ch4_11". ch4_11 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ch4_11 is a full-length clone,
10 including the entire coding sequence of a secreted protein (also referred to herein as "ch4_11 protein").

The nucleotide sequence of ch4_11 as presently determined is reported in SEQ ID NO:151, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ch4_11 protein
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:152. Amino acids 21 to 33 of SEQ ID NO:152 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 34. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated
20 from the remainder of the ch4_11 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ch4_11 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for ch4_11 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
25 FASTA search protocols. ch4_11 demonstrated at least some similarity with sequences identified as AA318160 (EST20431 Retina II Homo sapiens cDNA 5' end), R94133 (yt74g06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 276275 5'), and W27798 (37h1 Human retina cDNA randomly primed sublibrary Homo sapiens). The predicted amino acid sequence disclosed herein for ch4_11 was searched against the
30 GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ch4_11 protein demonstrated at least some similarity to sequences identified as L28819 (involucrin [Mus musculus]). The ch4_11 protein is the human homologue of the mouse K483_1 protein (see GenBank I80067 and I80068, GeneSeq

V09119, V09120, and W42028, and U.S. Patent No. 5,708,157). Based upon sequence similarity, ch4_11 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the ch4_11 protein sequence centered around amino acids 28, 189, and
5 280 of SEQ ID NO:152, respectively.

Clone "cn621_8"

A polynucleotide of the present invention has been identified as clone "cn621_8". cn621_8 was isolated from a human fetal brain cDNA library using methods which are
10 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cn621_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cn621_8 protein").

15 The nucleotide sequence of cn621_8 as presently determined is reported in SEQ ID NO:153, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cn621_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:154.

The EcoRI/NotI restriction fragment obtainable from the deposit containing
20 clone cn621_8 should be approximately 3500 bp.

The nucleotide sequence disclosed herein for cn621_8 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cn621_8 demonstrated at least some similarity with sequences identified as W18181 (IMAGE:20099 Soares infant brain 1NIB Homo sapiens cDNA clone
25 20099), W60570 (zd26g04.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 3418145'), W60661 (zd26g04.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone), and Z84474 (Human DNA sequence from PAC 111M5 on chromosome 6. Contains BBC1, RFP finger protein, EST, STS, tRNAs and polymorphic repeat). The predicted amino acid sequence disclosed herein for cn621_8 was searched against the GenPept and GeneSeq
30 amino acid sequence databases using the BLASTX search protocol. The predicted cn621_8 protein demonstrated at least some similarity to sequences identified as L35279 (BMP-1 [Homo sapiens]), U91963 (tollid-like (TLL) [Homo sapiens]), and X64414 (low density lipoprotein receptor [Mus musculus]). Based upon sequence similarity, cn621_8 proteins

and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the cn621_8 protein sequence centered around amino acid 220 of SEQ ID NO:154.

5 Clone "gy621_1"

A polynucleotide of the present invention has been identified as clone "gy621_1". gy621_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
10 analysis of the amino acid sequence of the encoded protein. gy621_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "gy621_1 protein").

The nucleotide sequence of gy621_1 as presently determined is reported in SEQ ID NO:155, and includes a poly(A) tail. What applicants presently believe to be the
15 proper reading frame and the predicted amino acid sequence of the gy621_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:156. Amino acids 11 to 23 of SEQ ID NO:156 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
20 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the gy621_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone gy621_1 should be approximately 3800 bp.

The nucleotide sequence disclosed herein for gy621_1 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. gy621_1 demonstrated at least some similarity with sequences identified as AA166536 (ms63h05.r1 Stratagene mouse embryonic carcinoma (#937317) Mus musculus cDNA clone 616281 5'), AA416723 (zu08a04.s1 Soares testis NHT Homo sapiens cDNA clone 731214 3'), and AA463756 (aa07a05.r1 Soares NhHMPu S1 Homo
30 sapiens cDNA clone 812528 5'). Based upon sequence similarity, gy621_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts at least one additional potential transmembrane domains within the

gy621_1 protein sequence of SEQ ID NO:156. The nucleotide sequence of gy621_1 indicates that it may contain one or more AC1 or AC2 repetitive elements.

Clone "hb1041_2"

5 A polynucleotide of the present invention has been identified as clone "hb1041_2". hb1041_2 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. hb1041_2 is a full-length
10 clone, including the entire coding sequence of a secreted protein (also referred to herein as "hb1041_2 protein").

The nucleotide sequence of hb1041_2 as presently determined is reported in SEQ ID NO:157, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the hb1041_2 protein
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:158. Amino acids 55 to 67 of SEQ ID NO:158 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 68. Due to the hydrophobic nature of the predicted leader/signal sequence, it may act as a transmembrane domain should the predicted leader/signal sequence not be separated
20 from the remainder of the hb1041_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone hb1041_2 should be approximately 2450 bp.

The nucleotide sequence disclosed herein for hb1041_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
25 FASTA search protocols. hb1041_2 demonstrated at least some similarity with sequences identified as AA050445 (mj21c12.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 476758 5'), AA087161 (mo11b05.r1 Life Tech mouse embryo 10 5dpc 10665016 Mus musculus cDNA clone 553233 5'), and W84558 (zd89h10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 356707 3'). The predicted amino acid sequence
30 disclosed herein for hb1041_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted hb1041_2 protein demonstrated at least some similarity to sequences identified as AB000459 (unnamed

protein product [Homo sapiens]). Based upon sequence similarity, hb1041_2 proteins and each similar protein or peptide may share at least some activity.

Clone "mh703_1"

5 A polynucleotide of the present invention has been identified as clone "mh703_1". mh703_1 was isolated from a human adult brain (thalamus) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. mh703_1 is a full-
10 length clone, including the entire coding sequence of a secreted protein (also referred to herein as "mh703_1 protein").

The nucleotide sequence of mh703_1 as presently determined is reported in SEQ ID NO:159, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the mh703_1 protein
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:160.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone mh703_1 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for mh703_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
20 FASTA search protocols. mh703_1 demonstrated at least some similarity with sequences identified as AA173536 (zp04e07.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 595428 5'), AA173577 (zp04e07.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 595428 3'), AA278788 (zs79a09.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 703672 5' similar to TR E189399 E189399 HYPOTHETICAL 51.4 KD
25 PROTEIN), and T26646 (Human gene signature HUMGS08893). The predicted amino acid sequence disclosed herein for mh703_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted mh703_1 protein demonstrated at least some similarity to sequences identified as R85881 (WD-40 domain-contg. YCW2 protein) and U80447 (similar to the beta
30 transducin family [Caenorhabditis elegans]). mh703_1 protein contains at least two beta-transducin family Trp-Asp repeat signature motifs, and also contains the WD-40 motif of G-proteins. Based upon sequence similarity, mh703_1 proteins and each similar protein or peptide may share at least some activity.

mh703_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 51 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

5 Clone "na461_19"

A polynucleotide of the present invention has been identified as clone "na461_19". na461_19 was isolated from a human adult brain (corpus callosum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis
10 of computer analysis of the amino acid sequence of the encoded protein. na461_19 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "na461_19 protein").

The nucleotide sequence of na461_19 as presently determined is reported in SEQ ID NO:161, and includes a poly(A) tail. What applicants presently believe to be the
15 proper reading frame and the predicted amino acid sequence of the na461_19 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:162. Amino acids 63 to 75 of SEQ ID NO:162 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 76. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
20 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the na461_19 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone na461_19 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for na461_19 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. na461_19 demonstrated at least some similarity with sequences identified as AA032203 (zf01d04.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 375655 3'), AA203707 (zx52c12.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 446134 5' similar to contains element MER2 repetitive element), AA262333
30 (zr70h11.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 668805 3'), AA318276 (EST20340 Retina II Homo sapiens cDNA 5' end), AA436588 (zv08e12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753070 5'), and T21229 (Human gene signature

HUMGS02545). Based upon sequence similarity, na461_19 proteins and each similar protein or peptide may share at least some activity.

Clone "na492_2"

5 A polynucleotide of the present invention has been identified as clone "na492_2". na492_2 was isolated from a human adult brain (corpus callosum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. na492_2 is a full-
10 length clone, including the entire coding sequence of a secreted protein (also referred to herein as "na492_2 protein").

The nucleotide sequence of na492_2 as presently determined is reported in SEQ ID NO:163, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the na492_2 protein
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:164. Amino acids 321 to 333 of SEQ ID NO:164 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 334. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated
20 from the remainder of the na492_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone na492_2 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for na492_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
25 FASTA search protocols. na492_2 demonstrated at least some similarity with sequences identified as AA514389 (nf57b05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:923985), H81154 (yu60f02.r1 Homo sapiens cDNA clone 230523 5'), and R89359 (yq05c05.s1 Homo sapiens cDNA clone 196040 3'). The predicted amino acid sequence disclosed herein for na492_2 was searched against the GenPept and GeneSeq amino acid
30 sequence databases using the BLASTX search protocol. The predicted na492_2 protein demonstrated at least some similarity to sequences identified as AB004534 (pi015 [Schizosaccharomyces pombe]). Based upon sequence similarity, na492_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer

program predicts two potential transmembrane domains within the na492_2 protein sequence, one centered around amino acid 350 and another around amino acid 370 of SEQ ID NO:164.

5 Clone "na669_10"

A polynucleotide of the present invention has been identified as clone "na669_10". na669_10 was isolated from a human adult brain (corpus callosum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis
10 of computer analysis of the amino acid sequence of the encoded protein. na669_10 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "na669_10 protein").

The nucleotide sequence of na669_10 as presently determined is reported in SEQ ID NO:165, and includes a poly(A) tail. What applicants presently believe to be the
15 proper reading frame and the predicted amino acid sequence of the na669_10 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:166. Amino acids 40 to 52 of SEQ ID NO:166 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 53. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
20 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the na669_10 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone na669_10 should be approximately 3300 bp.

The nucleotide sequence disclosed herein for na669_10 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. na669_10 demonstrated at least some similarity with sequences identified as AA035207 (zk27h11.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 471813 3'), AA429797 (zw57d10.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 774163 5'), AA512946 (nh91d01.s1 NCI_CGAP_Br1.1 Homo sapiens cDNA
30 clone IMAGE:965857), C20746 (HUMGS0004776, Human Gene Signature), and N33343 (yy08d08.s1 Homo sapiens cDNA clone 270639 3'). Based upon sequence similarity, na669_10 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within

the na669_10 protein sequence, one centered around amino acid 11 and another around amino acid 46 of SEQ ID NO:166.

Clone "co821_31"

5 A polynucleotide of the present invention has been identified as clone "co821_31". co821_31 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. co821_31 is a full-length
10 clone, including the entire coding sequence of a secreted protein (also referred to herein as "co821_31 protein").

The nucleotide sequence of co821_31 as presently determined is reported in SEQ ID NO:167, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the co821_31 protein
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:168. Amino acids 87 to 99 of SEQ ID NO:168 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 100. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated
20 from the remainder of the co821_31 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone co821_31 should be approximately 2400 bp.

The nucleotide sequence disclosed herein for co821_31 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
25 FASTA search protocols. co821_31 demonstrated at least some similarity with sequences identified as AA488906 (aa55a02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:8248105' similar to TR:G607003 G607003 BETA TRANSDUCIN-LIKE PROTEIN), L26690 (Mus musculus expressed sequence tag EST F101), N30002 (yx82e02.s1 Homo sapiens cDNA clone 268250 3'), R82926 (EST23j22 Clontech adult human fat cell library
30 HL1108A Homo sapiens cDNA clone 23j22), T20673 (Human gene signature HUMGS01889), and W44749 (zb98b11.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320829 3'). The predicted amino acid sequence disclosed herein for co821_31 was searched against the GenPept and GeneSeq amino acid sequence databases

using the BLASTX search protocol. The predicted co821_31 protein demonstrated at least some similarity to sequences identified as U51030 (Ydr267cp [Saccharomyces cerevisiae]). The predicted co821_31 protein also demonstrated at least some similarity to U92792 (general transcriptional repressor Tup1 [Schizosaccharomyces pombe]), L28125 (beta transducin-like protein (het-e1) [Podospora anserina]), and other proteins containing WD-40 motifs. Based upon sequence similarity, co821_31 proteins and each similar protein or peptide may share at least some activity.

Clone "dk329_1"

10 A polynucleotide of the present invention has been identified as clone "dk329_1". dk329_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dk329_1 is a full-length
15 clone, including the entire coding sequence of a secreted protein (also referred to herein as "dk329_1 protein").

The nucleotide sequence of dk329_1 as presently determined is reported in SEQ ID NO:169, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dk329_1 protein
20 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:170. Amino acids 71 to 83 of SEQ ID NO:170 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 84. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated
25 from the remainder of the dk329_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dk329_1 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for dk329_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
30 FASTA search protocols. dk329_1 demonstrated at least some similarity with sequences identified as AA147429 (zo39g07.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 589308 5' similar to WP T14G10.6 CE06452 LEUCOCYTE SURFACE ANTIGEN CD53 LINE), AA190572 (zp42h08.r1 Stratagene muscle 937209 Homo sapiens

cDNA clone 612159 5' similar to WP T14G10.6 CE06452 LEUCOCYTE SURFACE ANTIGEN CD53 LINE), AA234042 (zr51a05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 666896 3' similar to WP:T14G10.6 CE06452 LEUCOCYTE SURFACE ANTIGEN CD53 LINE), AA236262 (zr51a05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 5 666896 5' similar to WP:T14G10.6 CE06452 LEUCOCYTE SURFACE ANTIGEN CD53 LINE), N72328 (yv31f12.r1 Homo sapiens cDNA clone 244367 5' similar to SW A15_HUMANP41732 CELL SURFACE GLYCOPROTEIN A15), and W50192 (mb08d07.r1 Life Tech mouse brain Mus musculus cDNA clone 319597 5' similar to SW:CD53_HUMAN P19397 LEUCOCYTE SURFACE ANTIGEN CD53). The predicted 10 amino acid sequence disclosed herein for dk329_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dk329_1 protein demonstrated at least some similarity to sequences identified as Z68880 (T14G10.6 [Caenorhabditis elegans]) and a variety of membrane proteins involved in immune function. Based upon sequence similarity, dk329_1 proteins and 15 each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the dk329_1 protein sequence, centered around amino acids 31, 71, and 103 of SEQ ID NO:170, respectively.

dk329_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 18 kDa was detected in membrane fractions using SDS 20 polyacrylamide gel electrophoresis.

Clone "fx317_11"

A polynucleotide of the present invention has been identified as clone "fx317_11". fx317_11 was isolated from a human fetal brain cDNA library using methods which are 25 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fx317_11 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "fx317_11 protein").

30 The nucleotide sequence of fx317_11 as presently determined is reported in SEQ ID NO:171, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the fx317_11 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:172.

Amino acids 229 to 241 of SEQ ID NO:172 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 242. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated
5 from the remainder of the fx317_11 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fx317_11 should be approximately 1900 bp.

The nucleotide sequence disclosed herein for fx317_11 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
10 FASTA search protocols. fx317_11 demonstrated at least some similarity with sequences identified as AA505600 (nh93h11.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:966117), N47450 (yy89c09.r1 Homo sapiens cDNA clone 280720 5' similar to contains element PTR5 repetitive element), T64549 (Human activated platelet protein-2 APP-2 cDNA), and W52611 (zc49e02.r1 Soares senescent fibroblasts NbHSF Homo
15 sapiens cDNA clone 325658 5'). The predicted amino acid sequence disclosed herein for fx317_11 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted fx317_11 protein demonstrated at least some similarity to sequences identified as W15413 (Human activated platelet protein-2 APP-2) and W15414 (Human activated platelet protein-2 APP-2 alternatively spliced
20 variant). APP-2 protein is expressed on activated human platelets. Based upon sequence similarity, fx317_11 proteins and each similar protein or peptide may share at least some activity.

Clone "lp547_4"

25 A polynucleotide of the present invention has been identified as clone "lp547_4". lp547_4 was isolated from a human adult blood (peripheral blood mononuclear cells treated *in vivo* with granulocyte-colony stimulating factor) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of
30 computer analysis of the amino acid sequence of the encoded protein. lp547_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "lp547_4 protein").

The nucleotide sequence of lp547_4 as presently determined is reported in SEQ ID NO:173, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the lp547_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:174.

- 5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone lp547_4 should be approximately 1800 bp.

- The nucleotide sequence disclosed herein for lp547_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. lp547_4 demonstrated at least some similarity with sequences
10 identified as AA442560 (zv75g07.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 7595165' similar to TR:G436941 G436941 PHORBOLIN I). The predicted amino acid sequence disclosed herein for lp547_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted lp547_4 protein demonstrated at least some similarity to sequences identified as R58704 (Apo-B
15 RNA editing protein), U03891 (phorbolin I [Homo sapiens]), and U21951 (apolipoprotein B mRNA-editing component 1 [Mus musculus]). U03891 protein (phorbolin I) is upregulated in psoriatic keratinocytes. The predicted lp547_4 protein also contains a cytidine and deoxycytidylate deaminases zinc-binding region signature. Based upon sequence similarity, lp547_4 proteins and each similar protein or peptide may share at
20 least some activity. The TopPredII computer program predicts a potential transmembrane domain within the lp547_4 protein sequence, centered around amino acid 290 of SEQ ID NO:174; amino acids 278 to 290 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 291.

- lp547_4 protein was expressed in a COS cell expression system, and an expressed
25 protein band of approximately 41 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "lv310_7"

- A polynucleotide of the present invention has been identified as clone "lv310_7".
30 Clones were first isolated from a human adult thyroid cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or were identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. Probes derived

from these cDNAs were then used to isolate lv310_7 from a human adult brain cDNA library. lv310_7 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "lv310_7 protein").

The nucleotide sequence of lv310_7 as presently determined is reported in SEQ ID NO:175, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the lv310_7 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:176. Amino acids 269 to 281 of SEQ ID NO:176 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 282. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the lv310_7 protein.

Another possible lv310_7 reading frame and predicted amino acid sequence, encoded by base pairs 1619 to 2188 of SEQ ID NO:175, is reported in SEQ ID NO:283.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone lv310_7 should be approximately 3650 bp.

The nucleotide sequence disclosed herein for lv310_7 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. lv310_7 demonstrated at least some similarity with sequences identified as N37001 (yy40a01.s1 Homo sapiens cDNA clone 273672 3'), R56228 (yg90d01.s1 Homo sapiens cDNA clone 40958 3'), and R56310 (yg90d01.r1 Homo sapiens cDNA clone 40958 5'). The predicted amino acid sequence disclosed herein for lv310_7 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted lv310_7 protein demonstrated at least some similarity to sequences identified as U24223 (alpha-CP1 [Homo sapiens]). Based upon sequence similarity, lv310_7 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts 10 potential transmembrane domains within the lv310_7 protein sequence, centered around amino acids 100, 130, 160, 210, 280, 490, 520, 600, 690, and 750 of SEQ ID NO:176, respectively.

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Clone "nq34_12"

A polynucleotide of the present invention has been identified as clone "nq34_12". nq34_12 was isolated from a human adult blood (erythroleukemia TF-1) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. nq34_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "nq34_12 protein").

The nucleotide sequence of nq34_12 as presently determined is reported in SEQ ID NO:177, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the nq34_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:178. Amino acids 287 to 299 of SEQ ID NO:178 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 300. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the nq34_12 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone nq34_12 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for nq34_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. nq34_12 demonstrated at least some similarity with sequences identified as AA126375 (zl86c06.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 511498 5'), AA446675 (zw84a08.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 783638 5'), AA448974 (zx07d05.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 785769 5' similar to SW YND0_YEAST P40344 HYPOTHETICAL 35.9 KD PROTEIN IN RPC34-CSE2 INTERGENIC REGION), R57902 (F6699 Fetal heart Homo sapiens cDNA clone F6699 5' end), and X07453 (Plasmodium falciparum 11-1 gene part 1). The predicted amino acid sequence disclosed herein for nq34_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted nq34_12 protein demonstrated at least some similarity to sequences identified as X77395 (N2040 gene product [Saccharomyces cerevisiae]). Based

upon sequence similarity, nq34_12 proteins and each similar protein or peptide may share at least some activity.

nq34_12 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 34 kDa was detected in membrane fractions using SDS
5 polyacrylamide gel electrophoresis.

Clone "pj154_1"

A polynucleotide of the present invention has been identified as clone "pj154_1". pj154_1 was isolated from a human fetal carcinoma (NTD2 cells treated with retinoic acid
10 for 23 days) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pj154_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pj154_1 protein").

15 The nucleotide sequence of pj154_1 as presently determined is reported in SEQ ID NO:179, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pj154_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:180. Amino acids 13 to 25 of SEQ ID NO:180 are a predicted leader/signal sequence, with the
20 predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pj154_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing
25 clone pj154_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for pj154_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pj154_1 demonstrated at least some similarity with sequences identified as AA223153 (zr07g12.r1 Stratagene NT2 neuronal precursor 937230 Homo
30 sapiens cDNA clone 650854 5'), AA223170 (zr07g12.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 650854 3' similar to contains Alu repetitive element), H16627 (ym26d04.r1 Homo sapiens cDNA clone 49469 5'), and Z44660 (H. sapiens partial cDNA sequence; clone c-26d11). Based upon sequence similarity, pj154_1 proteins and

each similar protein or peptide may share at least some activity. The nucleotide sequence of pj154_1 indicates that it may contain an Alu repetitive element.

Clone "pk147_1"

5 A polynucleotide of the present invention has been identified as clone "pk147_1". pk147_1 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pk147_1 is a
10 full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pk147_1 protein").

The nucleotide sequence of pk147_1 as presently determined is reported in SEQ ID NO:181, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pk147_1 protein
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:182. Amino acids 16 to 28 of SEQ ID NO:182 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 29. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated
20 from the remainder of the pk147_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pk147_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for pk147_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
25 FASTA search protocols. pk147_1 demonstrated at least some similarity with sequences identified as AA126920 (zl23h01.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 502801 3'), AA406448 (zv12f07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753445 5'), and R51886 (yg78c03.s1 Homo sapiens cDNA clone 39574 3'). Based upon sequence similarity, pk147_1 proteins and each similar protein or peptide may share at
30 least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the pk147_1 protein sequence centered around amino acid 37 of SEQ ID NO:182.

Clone "pt127_1"

A polynucleotide of the present invention has been identified as clone "pt127_1". pt127_1 was isolated from a human adult blood (lymphoblastic leukemia MOLT-4) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pt127_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pt127_1 protein").

The nucleotide sequence of pt127_1 as presently determined is reported in SEQ ID NO:183, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pt127_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:184. Amino acids 8 to 20 of SEQ ID NO:184 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pt127_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pt127_1 should be approximately 2600 bp.

The nucleotide sequence disclosed herein for pt127_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pt127_1 demonstrated at least some similarity with sequences identified as AA081843 (zn19g10.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 547938 5') and R39258 (yc91h08.s1 Homo sapiens cDNA clone 23514 3'). Based upon sequence similarity, pt127_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential transmembrane domains within the pt127_1 protein sequence centered around amino acids 60, 100, 130, 190, and 240 of SEQ ID NO:184.

Clone "qo115_13"

A polynucleotide of the present invention has been identified as clone "qo115_13". qo115_13 was isolated from a human adult brain (corpus callosum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No.

5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qo115_13 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qo115_13 protein").

5 The nucleotide sequence of qo115_13 as presently determined is reported in SEQ ID NO:185, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qo115_13 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:186. Amino acids 29 to 41 of SEQ ID NO:186 are a predicted leader/signal sequence, with the
10 predicted mature amino acid sequence beginning at amino acid 42. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qo115_13 protein.

 The EcoRI/NotI restriction fragment obtainable from the deposit containing
15 clone qo115_13 should be approximately 1200 bp.

 The nucleotide sequence disclosed herein for qo115_13 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the database. The nucleotide sequence of qo115_13 indicates that it may contain repetitive elements.

20

Deposit of Clones

 Clones bd306_7, fj283_11, fk317_3, k213_2x, na316_1, nf93_20, np164_1, pe204_1, ya1_1, and yb8_1 were deposited on November 26, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.)
25 as an original deposit under the Budapest Treaty and were given the accession number 98599, from which each clone comprising a particular polynucleotide is obtainable. Clone fj283_6 was deposited on 17 November, 1998 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98988.

30 Clones am856_3, am996_12, cc69_1, cc162_1, if87_1, nn103_4, np206_8, nt746_4, pe286_1, and yb7_1 were deposited on December 4, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.)

as an original deposit under the Budapest Treaty and were given the accession number 98600, from which each clone comprising a particular polynucleotide is obtainable.

Clones am728_60, bf377_1, cw354_1, nm134_4, yb11_1, and yc2_1 were deposited on December 19, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98621, from which each clone comprising a particular polynucleotide is obtainable.

Clones ff168_12, ls9_1, na1010_1, nf87_1, nh796_1, nn229_1, and np156_1 were deposited on December 31, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98623, from which each clone comprising a particular polynucleotide is obtainable.

Clones bg570_1, bi120_2, bn594_1, en554_1, na474_10, nn16_10, np189_9, ny226_1, pe159_1, and pj314_8 were deposited on January 7, 1998 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98629, from which each clone comprising a particular polynucleotide is obtainable.

Clones bp870_2, bx141_2, cw272_7, nh328_5, nm214_3, nn320_2, pp392_3, ya13_1, yb37_1, and yb39_1 were deposited on January 8, 1998 with the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98630, from which each clone comprising a particular polynucleotide is obtainable. Clone bp870_1 was deposited on April 7, 1998 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98724, from which deposit the bp870_1 clone comprising a particular polynucleotide is obtainable.

Clones bd577_1, bv280_3, co315_3, ij226_6, nf443_1, nt429_1, pe503_1, pe834_6, ya10_1, and yb40_1 were deposited on January 13, 1998 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98631, from which each clone comprising a particular polynucleotide is obtainable.

Clones cs756_2, ew150_1, gg894_13, it217_2, ml235_2, mt24_2, pe584_2, pj323_2, yb24_1, and yb44_1 were deposited on January 22, 1998 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 5 98636, from which each clone comprising a particular polynucleotide is obtainable.

Clones bn69_15, cb110_1, ch4_11, cn621_8, gy621_1, hb1041_2, mh703_1, na461_19, na492_2, and na669_10 were deposited on January 30, 1998 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the 10 accession number 98647, from which each clone comprising a particular polynucleotide is obtainable.

Clones co821_31, dk329_1, fx317_11, lp547_4, lv310_7, nq34_12, pj154_1, pk147_1, pt127_1, and qo115_13 were deposited on February 18, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) 15 as an original deposit under the Budapest Treaty and were given the accession number ATCC 98663, from which each clone comprising a particular polynucleotide is obtainable.

All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 20 1.806.

Each clone has been transfected into separate bacterial cells (*E. coli*) in these composite deposits. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or 25 pNOTs vector depicted in Figures 1A and 1B, respectively. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* 19: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* 9: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13 origin of 30 replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper

orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

- 5 An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

10

	<u>Clone</u>	<u>Probe Sequence</u>
	bd306_7	SEQ ID NO:187
	fj283_11	SEQ ID NO:188
	fj283_6	SEQ ID NO:197
15	fk317_3	SEQ ID NO:189
	k213_2x	SEQ ID NO:190
	na316_1	SEQ ID NO:191
	nf93_20	SEQ ID NO:192
	np164_1	SEQ ID NO:193
20	pe204_1	SEQ ID NO:194
	ya1_1	SEQ ID NO:195
	yb8_1	SEQ ID NO:196
	am856_3	SEQ ID NO:199
	am996_12	SEQ ID NO:200
25	cc69_1	SEQ ID NO:201
	cc162_1	SEQ ID NO:202
	if87_1	SEQ ID NO:203
	nn103_4	SEQ ID NO:204
	np206_8	SEQ ID NO:205
30	nt746_4	SEQ ID NO:206
	pe286_1	SEQ ID NO:207
	yb7_1	SEQ ID NO:208
	am728_60	SEQ ID NO:209

	cw354_1	SEQ ID NO:210
	nm134_4	SEQ ID NO:211
	yb11_1	SEQ ID NO:212
	yc2_1	SEQ ID NO:213
5	ff168_12	SEQ ID NO:214
	ls9_1	SEQ ID NO:215
	na1010_1	SEQ ID NO:216
	nf87_1	SEQ ID NO:217
	nh796_1	SEQ ID NO:218
10	nn229_1	SEQ ID NO:219
	np156_1	SEQ ID NO:220
	bi120_2	SEQ ID NO:221
	na474_10	SEQ ID NO:222
	nn16_10	SEQ ID NO:223
15	np189_9	SEQ ID NO:224
	ny226_1	SEQ ID NO:225
	pe159_1	SEQ ID NO:226
	pj314_8	SEQ ID NO:227
	bp870_1	SEQ ID NO:228
20	bx141_2	SEQ ID NO:229
	cw272_7	SEQ ID NO:230
	nh328_5	SEQ ID NO:231
	nm214_3	SEQ ID NO:232
	nn320_2	SEQ ID NO:233
25	pp392_3	SEQ ID NO:234
	yb37_1	SEQ ID NO:235
	bd577_1	SEQ ID NO:236
	bv280_3	SEQ ID NO:237
	co315_3	SEQ ID NO:238
30	ij226_6	SEQ ID NO:239
	nf443_1	SEQ ID NO:240
	nt429_1	SEQ ID NO:241
	pe503_1	SEQ ID NO:242

	pe834_6	SEQ ID NO:243
	yb40_1	SEQ ID NO:244
	cs756_2	SEQ ID NO:245
	ew150_1	SEQ ID NO:246
5	gg894_13	SEQ ID NO:247
	it217_2	SEQ ID NO:248
	ml235_2	SEQ ID NO:249
	mt24_2	SEQ ID NO:250
	pe584_2	SEQ ID NO:251
10	pj323_2	SEQ ID NO:252
	yb24_1	SEQ ID NO:253
	bn69_15	SEQ ID NO:254
	cb110_1	SEQ ID NO:255
	ch4_11	SEQ ID NO:256
15	cn621_8	SEQ ID NO:257
	gy621_1	SEQ ID NO:258
	hb1041_2	SEQ ID NO:259
	mh703_1	SEQ ID NO:260
	na461_19	SEQ ID NO:261
20	na492_2	SEQ ID NO:262
	na669_10	SEQ ID NO:263
	co821_31	SEQ ID NO:264
	dk329_1	SEQ ID NO:265
	fx317_11	SEQ ID NO:266
25	lp547_4	SEQ ID NO:267
	lv310_7	SEQ ID NO:268
	nq34_12	SEQ ID NO:269
	pj154_1	SEQ ID NO:270
	pk147_1	SEQ ID NO:271
30	pt127_1	SEQ ID NO:272
	qo115_13	SEQ ID NO:273

In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

The design of the oligonucleotide probe should preferably follow these parameters:

- (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;
- (b) It should be designed to have a T_m of approx. 80 ° C (assuming 2° for each A or T and 4 degrees for each G or C).

The oligonucleotide should preferably be labeled with γ -³²P ATP (specific activity 6000 Ci/mmol) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4e+6 dpm/pmol.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 μ l of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100 μ g/ml. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 μ g/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 μ g/ml of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix

at a concentration greater than or equal to 1×10^6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are

derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can
5 be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of
10 the organism from which the gene was isolated.

The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible to determine the corresponding chromosomal location for a disclosed
15 polynucleotide by identifying significantly similar nucleotide sequences in public databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession number.
20 Searches using the GenBank accession numbers of these public database sequences can then be performed at an Internet site provided by the National Center for Biotechnology Information having the address <http://www.ncbi.nlm.nih.gov/UniGene/>, in order to identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters" so identified will already have been mapped to particular chromosomal sites.

25 Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* **15**(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* **62**(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* **58**: 1-39; all of which are incorporated by reference herein). Transgenic animals that have
30 multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are

stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein).

5 In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of
10 transposable elements (Plasterk, 1992, *Bioessays* 14(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059;
15 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the
20 protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and
25 transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of transmembrane domains in an amino acid sequence, domains which are described by the location of the center of the transmembrane domain, with at least ten transmembrane
30 amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60%

sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

10 In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle *ed.*, *Methods in Enzymology* 266: 460-480; Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of*
15 *Molecular Biology* 215: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, *Nature Genetics* 3: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci. USA* 90: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX
20 platforms can be downloaded from <ftp://blast.wustl.edu/blast/executables>. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely used for
25 commercial, nonprofit, or academic purposes. In all search programs in the suite -- BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length
30 one is Q=9 for proteins and BLASTP, and Q=10 for BLASTN, but may be changed to any integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue

penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. Any combination of values for Q and R can be used in order
5 to align sequences so as to maximize overlap and identity while minimizing sequence gaps. The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or
10 polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence
15 identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from the
20 sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus*, *Hylobates concolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, *Aotus*
25 *trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*, *Cricetulus griseus*, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species
30 (O'Brien and Seuánez, 1988, *Ann. Rev. Genet.* 22: 323-351; O'Brien *et al.*, 1993, *Nature Genetics* 3:103-112; Johansson *et al.*, 1995, *Genomics* 25: 682-690; Lyons *et al.*, 1997, *Nature Genetics* 15: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* 13(10): 393-399; Carver and Stubbs, 1997, *Genome Research* 7:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least
5 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences
10 provided herein and screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides that hybridize under reduced
15 stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least
20 as stringent as, for example, conditions M-R.

	Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
5	A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	DNA:DNA	<50	T _B *; 1xSSC	T _B *; 1xSSC
	C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	<50	T _D *; 1xSSC	T _D *; 1xSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	RNA:RNA	<50	T _F *; 1xSSC	T _F *; 1xSSC
10	G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	DNA:DNA	<50	T _H *; 4xSSC	T _H *; 4xSSC
	I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	<50	T _J *; 4xSSC	T _J *; 4xSSC
	K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	<50	T _L *; 2xSSC	T _L *; 2xSSC
15	M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	<50	T _N *; 6xSSC	T _N *; 6xSSC
	O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
	P	DNA:RNA	<50	T _P *; 6xSSC	T _P *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	<50	T _R *; 4xSSC	T _R *; 4xSSC

*: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

†: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6(log₁₀[Na⁺]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the

hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial

strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art

given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

5 The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors
10 suitable for introduction of DNA).

Research Uses and Utilities

 The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant
15 protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA
20 sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression
25 patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those described in Gyuris *et al.*, 1993, *Cell* 75:
30 791-803 and in Rossi *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* 94: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may

induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK. The activity of a protein of the invention may, among other means, be measured by the following methods:

- 10 Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986;
- 15 Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

- Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

- Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983;
- 25 Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991;
 - 30 Smith et al., *Proc. Natl. Acad. Sci. U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols*

in *Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

- 5 Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience
- 10 (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc.Natl.Acad.Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

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Immune Stimulating or Suppressing Activity

- A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies
- 20 and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral,
- 25 bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.
- 30 Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis,

myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for
5 example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction
10 of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is
15 distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without
20 limitation B lymphocyte antigen functions (such as, for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated
25 through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-
30 1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an

immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or
5 tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in
10 rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the
15 effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production
20 of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which
25 may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune
30 encephalitis, systemic lupus erythmatosis in MRL/*lpr/lpr* mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune
5 response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient
10 by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic
15 acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function
20 (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides.
25 For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used
30 to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the

transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro*

antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *J. Immunol.* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., *Cytometry* 13:795-808, 1992; Gorczyca et al., *Leukemia* 7:659-670, 1993; Gorczyca et al., *Cancer Research* 53:1945-1951, 1993; Itoh et al., *Cell* 66:233-243, 1991; Zacharchuk, *Journal of Immunology* 145:4037-4045, 1990; Zamai et al., *Cytometry* 14:891-897, 1993; Gorczyca et al., *International Journal of Oncology* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., *Blood* 84:111-117, 1994; Fine et al., *Cellular Immunology* 155:111-122, 1994; Galy et al., *Blood* 85:2770-2778, 1995; Toki et al., *Proc. Nat. Acad. Sci. USA* 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even

marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama

et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for
5 generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also
10 exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting
15 differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described
20 in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in:
Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year
25 Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related
30 activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful

as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

10 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc.*
15 *Natl. Acad. Sci. USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or
20 neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed
30 movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their

ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

10 The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and
15 Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

20 Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the
25 inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic
30 inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over

production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Cadherin/Tumor Invasion Suppressor Activity

5 Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering
10 skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The cadherin domains bind calcium to form their tertiary structure and
15 thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this recognition site can change the specificity of a cadherin so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

20 E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to
25 their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention
30 encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the
5 inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block the
10 adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

15 Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present
20 invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995;
25 Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities.
30 A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by

inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

5 Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, 10 weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, 15 carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic 20 lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another 25 material or entity which is cross-reactive with such protein.

ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a 30 pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the

effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, 5 IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize 10 side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

15 A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex 20 of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins 25 including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other 30 molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other

pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or

cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's

response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100
5 mg (preferably about 0.1mg to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is
10 contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal
15 and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J.
20 Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression
25 of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the
30 composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue

damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

10 The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and
15 polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of
20 material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

 Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In
25 some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose,
30 ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropylmethylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer

and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

